

FIGURE 1

ACTGCACCTCGGTTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCG
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCGCTGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAACGCCACGCCCTGCCACCAGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACAACTTGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCAGGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGGAGCAGACA
GGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGCCTACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCGTGTGTGCCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCACACAGCT
GCCCTCCCGCAAGACCTGTAATGTGCCGACTTACCCCTTAAATTATTCAAGAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAAATCAGG
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAACG
TTGCCGCCATGGCCAATTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCAGCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCGGATCGGAATTAAATTGCCGCAGCACCATGCCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGCGGAAAGAACCAAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKNFGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEARQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGSLTNRDCGECEVGWLDE
GACVDVDECAAEP PCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCAGCGCGCCAGCCGTCTAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCATGGCCCAGGAGCGCCTTC
CCTGCCGCCCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCAGGGCGGAGGC
CGGCCGCCAGGAGGAGGCCTGTACCTATGGATCGATGCTACCAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTCTATGAATTCTGTCCCTGGCCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCTTGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAGCTGAGTGCAGGCCAGGCGGGTGCAGAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGTGTCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACGTGACAAAGCAAACGCTCAACCACCTGCTTAAATGGAGGGACC
TGTTCCTACCCCTGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACACCCGTGCAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTCAAAGCCTGCTGCGAGCCTGGCTGTGGTCACAT
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCCTCACTAAAAAGGCCAGGGAGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCACTGTTCAAGTGGCAGATTTATATTGTCAATTGA
TCAGGTTAAAATTTCAGTGTGAGTTGGCAGATTTCAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTACAGCATTCAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
GTTGTTACATTAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGACCT
TTACCAATTCCAGAGATTCACTGTTCAAGGAGATTTAAACACTGTGGTAGTGGCATT
AAACAATATAATATATTCTAACACAAATGAAATAGGAATATAATGTATGAACCTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTACCTAACAAACATT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAAAA
AAAAAAAAAAAAAAAGGGCGGCCGCACTTAGAGTCGACCTGCAGAAGCTTGGC
GCCATGGCCCAACTGTTATTGCAGCTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCCGGCGTCGAGAGCCAGGAGGCCAGGGAGGCCAGGAGGCCAGGAGGCCACCATGTGGCGATGTCCACTGGGCTAC
TGCTGTTGCTGCCGCTGGCTGCCACTTGGCTCTGGCTGGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCCAGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGCCGTGCCAGCACTGTGCCCTGCCACTCTGGGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGCTCCGACTGCTGCCCTGACTTCTGGACTTC
TGCCTCGGCGTGCCACCCCCCTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTTGGAACGTACTGGACAACGTAAACCGTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCCCTGGATGAGGGCATTGCTACCGCTGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGCTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAAGTGGCCAACCTGATTGATGAGCCTCTTGA
CCAAGGCAACTGTGAGGCTCTGGCCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCTGTGCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCCGTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTCGGGCGTGAAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGACAGCCGAGCCATGGTCGGGGCAAGCGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGGCCCTGTCACGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGAGCTCAAATACTGGAAGTGCAGGCCACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGCCACTTCCGATCGTGCAGGCCGTCATGAGTGCACATCGAG
AGCTTCTGTGCTGGCGTCTGGGCGCGTGGCATGGAGGACATGGTCATCACTGAGGCTG
CGGGCACACGCCGGGTCCGGCTGGATCCAGGCTAACGGCCGGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTGCCGACAGAGCCGGGCGCAGGCCGGCGCCAGGGCGCTAAT
CCCGCGCGGGTCCGCTGACGCAGGCCCGCCTGGAGGCCGGCAGGGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGACGGGGCAGGGCCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCCTCTGGCGCCCCACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCG
TTGCCAGGTGGAGTGCAGTGGCCATCAGGGCTACTGTAACCTCCGACTCCTGGTTCA
AGTACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACTGGC
TAATTTTGATTTTGTAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCAACT
CCTGGCTCAAGCGGTCCACCTGCCTCCGCCTCCAAAGTGCAGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTTCACTGTTTAAAAA
TAAAACCAAAGTATTGATAAAAAAAAAAA

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pi: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTGGGACACATNACGCCCTGTCCTTNGCCCCAGAACCTGCTGTCTTGACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTCGCTGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACGCCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTCCTATAACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGA~~CTGCCTGCAGGTGGAGAA~~ACTGCACCCAGCTGGGG
GAGCAGTGCTGGACC~~CGCGCATCCGCG~~CAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGA~~ACTGCGTGG~~ATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCC~~TGCTGCT~~CTGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGT~~GCC~~CAGGCCTCTGTGCCACTCCTCACAGACCTG
GCC~~CA~~GTGGGAGCCTGT~~CTGGT~~CC~~TGAGG~~CACATCCTAACGCAAGTCTGACC~~ATGT~~TATGT
CTGCACCCCTGTCCCCCAC~~CC~~CTGACCC~~CT~~CCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGT~~GACACAGA~~TCCGCC~~TG~~CAGATGGCC~~CTCCA~~ACCC~~CT~~CTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCC~~TTAAC~~CC~~TG~~CTCAGGCACCTCTCCCCCAGGAAGC~~CTT~~
CCCTGCC~~CCACCC~~CATCTATGACTTGAGCCAGGTCTGGTCC~~GTGGT~~GTCCCCG~~CACCC~~CAGCA
GGGGACAGGC~~ACTCAGG~~AGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAA~~CTGGA~~
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCC~~TGGAGG~~C~~CTGGAGG~~A
GGGCCAGGC~~CTCACATT~~CGTGGGCTCC~~CTGA~~ATGGCAGC~~CTGAG~~CACAGCGTAGGCC~~CTT~~
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACCGCGTCCGAACCTCTCCAGCGATGGGAGGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCAGGCGAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCAACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGGTTCACGGAGATCGTGGAGAACAACTATACTGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGGCGCAGGGCGGCCAGGCTCCAGGCCAGCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGGCCCTCTACCAAGGCCAGCTGCCCTCCCCAACCACGC
CGAGAACAGAACAGCAGTTGAGTTGTGGCTCCGCCACCCGCCAGAACGCGCACAC
GGCGGCCAGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGCCGCTCCC
CACCCCTTCCCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCAGTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCTCCAGCCCCAAACTCCTCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAGGAAAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGCCAGGCCTGCACCCACCCCCACTCCCAGCCC
CGGAATAAAACCATTTCTGC

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FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHKVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIKGPSGKS KDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCATCCAGT
CATTGGATTTGCTGTTATTTTTCTTTCTTTCCCACCATGTATTTAT
TTCCGTACTTCAGAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCCT
GAAGTCTTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTCACCTGGCCTGCC
CTAGTGTGTGCCGCTCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACACAAACAAACCAATTAAATGC
TGGATTTCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTCAGAGTTCTCCATTGAGGAAAAC
AATATTAGACCAATTTCACGGGCTGCTTGCCCCAGCTTGAGGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAGACGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTGTCTAAGAATCACCTGAGCAGTGTGCCTTGGGCTTCCGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTCAGGGAACCTCCTGACCAACAAGGGTATGCCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTCAGTACGCTTCCAGGAC
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAAGAT
AAACCACATTCTTGCAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTTGATAATCTCTCCAACTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTGACTGAGTATTAAATGGGTACAGAAATGGCTCAA
ATATATCCCTTCATCTCAACGTGCCGGGTTCATGTGCCAAGGTCTGAACAAAGTCCGGG
GGATGGCGTCAGGGAAATTAAATGAATTTGTCCTGCTCCACACGACCCCCGGCTG
CCTCTTCAACCCAGCCCCAAGTACAGCTTCCGACACTCAGCCTCCCACCCCTCTAT
TCCAAACCTAGCAGAAGCTACACGCCCTCAACTCCTACACATGAAACTTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACCTATTCTGAACGGATCCAGCTCTATC
CATTGTAATGATACTCCATTCAAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATA
CAAACTCACATGGGTGAAATGGGCCACAGTTAGTAGGGGCATCGTTAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGTTTAACCTACCGCGCGTAGAAGACACCAATTGTTAGGAGC
CACCAACCATGCCCTTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGCTTGATGGGGCGCGGTGATATT
GTGCTGGTGGTCTTGCCTAGCGTCTTGTGCTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGCCGGAAAGATGATTATGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCTGGAGATGACAGAAACCGAGTTTCAGATCGTCTCTTAAATAACGAT
CAAACCTTAAAGGAGATTTCAGACTGCAGCCATTACACCCAAATGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGAACGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGCACATAAGACACGCAGATTACATTGATAATGTACACAGATGCAT
TTGTCATTGAATACTCTGTAATTATAACGGTGTACTATATAATGGGATTAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKS~~WLI~~ISLGLYSQVS~~KLL~~ACPSVCRCDRNFVYCNERSLT~~S~~VPLGIP
EGVT~~VLYL~~HNNQINNAGFPAELHN~~V~~QSVHTVYLYGNQLDEFPMNL~~P~~KNVRVL~~H~~LQENNIQTI
SRAALAQLLKLEELHLD~~D~~NS~~I~~STVGVEDGAFREAISL~~KLL~~FLSKNHLS~~S~~VPVGLPVDLQELR
VDENRIA~~V~~ISDMAFQNLTS~~L~~ERLIVDGNLLTNKGIAEGTFS~~H~~LT~~K~~KEFSIVRN~~N~~LSH~~PP~~D
LPGTHLIRLYLQDNQINHIPLTA~~F~~SNLRKLERLDISNNQLRMLTQGVFDNL~~S~~NL~~K~~QLT~~A~~NN
PWFCDCS~~I~~KWVTEWLKYIPSSLNVRGFM~~C~~QGPEQVRGM~~A~~RELNM~~N~~LLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPT~~T~~SKLPTIPWDGRERVT~~P~~P~~I~~SERIQLSIHFVND
TSIQVSWL~~S~~LSFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSVNLEPRSTYRICLVPL
DAFNYRAVE~~D~~TICSEATTHASYL~~N~~NGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKD~~N~~SILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHI~~P~~NNMRYCNS~~S~~VPDLEH~~C~~HT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGGGGGAGACAGAGGCAGAGGCAGAACGCTGGGGCTCCGTCTCGCCTCCCACGAGCG
ATCCCCGAGGAAGGCCGCGCCCTCGCGAGGCAGAAGAGGGCGAGGAGGAAGACCCGGGTTGGCTCGGCCCCCTGCC
TCGCTTCCCAGGCAGGGCTGCAGCCTTGCCCCCTCTGCTCGCTTGAAATGGAAAAGATGCTCGCAGGCT
GCTTCTGCTGATCCTCGACAGATCGCCTCCTCCCTGCGAGGGCAGGGAGCGGTACGTGGAGGTCCATCT
CTAGGGCAGACACCGCTCGAACCCACCCGAGACGGCCCTCTGGAGAGTTCTGTGAGAACACAAGCCAGACC
TGGTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGAGA
TCTTGCAATTCTTGACATTGGCTCTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGGATCTGTCCACGG
GCACCATGACTGGCTGGCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGTATAATGATCGACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCACGGGACACGGGATCCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCACACACCTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCCTCTGTGGCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACACTTGCGAGAACATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCTCGCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGACTACTGTGCCCTCAGAAAACCACGGATGTGAAC
ATGAGTGTGTAATGCTGATGGCTCTACCTTGCCAGTGCCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGACACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCAGTGACCAACTGTGCAAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGGAGGATTCTCGCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACCGAGGACCTCAAGACCTGCTCCGGGATTACTGCCCTGTGAGTGACCATGGTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCCCTGTGAGTGTGCTGAGGGACACGTGCTCCGAGCGATGGGAAGACGTGTG
CAAATGGACTCTGTGCTCTGGGGACACGGTTGTGAAGATGGAAAACCTGCAAGAAGGAAAGATGCTGCCAAGCTATA
ACCATGGCTGTGAACACATTGTGTAACAGTGACGACTCATACAGTGCAGTGCTGGAGGGATTCCGGCTCG
CTGAGGATGGGAACGCTGCCAGGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCGAACACATTGTGTTA
ATAATGGGAATTCTACATCTGCAAATGCTCAGAGGATTGTTCTAGCTGAGGACGGAGACGGTCAAGAAAT
GCACTGAAGGCCAATTGACCTGGCTTGATCGATGGATCCAAGAGTCTGGAGAAGAGAATTGAGGTCG
TGAAGCAGTTGTCACTGGAATTATAGATTCCCTGACAATTCCCCAAAGCCGCTCGAGTGAGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTCAACTCAGCCAAGACATGAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAGGGCTCATGACTGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG
GAGAAGGGCCAGGCCCTTCCACAAGGGTGCAGACGCCATTGTTGTCACCGACGGACGGCTCAGGATG
ACGTCCTCGAGTGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGGCCACAAACAAGCATCTTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTGAAGAAACTCAAGAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCAGTCACCATAAAATATCCAAGACCTACTTT
CCTGTTCTAAATTGCGAGTGCAACACAGATATCTGTTGAAAGAAGACAATCTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTCAGGAAGGCCCTTGGAAGGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCACAGGAAAGAAGTAAAGAAAATTACACAGGCTTAGAAGAAATGACACAGAGAATGGAGGCC
TGGAAAATCGCTGAGATACAGATGAAGATTAGAAATCGCGACACATTGTTAGTCATTGTATCAGGATTACAAT
GAAGCAGTGAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGAAGTAAACAAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATAACACTAACTTGTATAAATTATCTAGGAAAAAAACCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTTAATATACTGTGGACAC
AACTGCTTCTGCCCTACCTGCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTAATTGTGGAACAAGTTGATTTTACATATAATTAAATTCAACACTTCAG

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSGRSISRGRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE
HSCVSSEDASFVCQCPEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRILA
EDGKRCRKDVCKSTHGCEHICVNNNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDENNLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGTGTCAAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGGGCTGGCGCCCTGACTCCGTCCCGCCAGGGAGGGC
CATGATTCCCTCCGGGCCCCTGGTGACCAAACTTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGGGGCCAGCTGCAACTGCACCTGCCGCCAACGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGGAGCTGTTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCAACGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTCTGGTAT**TGATGAC**
CCCACCACTATTGGCTAAAGGATTGGGTTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCCTCAAGTCAGTAAGACCTAACAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCAGTCAGTGAGTCAGCTCCAGGC
CCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAAGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTTGTTTCATTGCAAATTAAATAAGATAACATAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKP
AVQYQ WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGT
AQCNCVTLEVSTGP
GAA VVAGAVVGT
LVGLGLLAGLVLLYHRRGKALEEPANDIKA
IAPIR
TLPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPS
PRLPTTDGAHPQP
ISPIPGGVSSSGLSR
MGAVPVMVPAQS
QAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAAATGAAACGCCTCCGCTCCTAGTGGTTTTCCACTTG
TTGAATTGTCCTATACTCAAAAATTGCACCAAGACACCTTGTCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAAAAACTTAAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAA
CTATCTCAGCCAAGGACACCCTTCTAACTCAACTCTTACTGAATTGAAAAACCGTGAAT
AATTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGITGCATTTTATTATA
AGAGTATTGGTCTTGCTTCCATCATCTGACAACTCTTATTGAAACCTCAAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTCACAGATA
GGTATAGGAGTCTATGTGATTTGGAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTTAATCACCT
GACACATTTTGCAATTTTGATGTCCTCTGGTCCATTGGTATTAAAGATTATAAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTTTGCTTGCATATGCATT
ACCTTCTGGTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCAAAAAATCTTGCTG
TAGCCTATTCTTGCTGAACTTGTTTCTTGTGGGATCAATCAAATACTAAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTCTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATGTTTGTTGGGTGCATCTACAACAAAGGATT
CAAGAATTTTTATCTTGGCTATCTAGGCCACGCCGTGGTAGTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACACCAAAGTATGTTGGCTAGCACCGAAAACAACTTTATT
TGGAGTTTTATAGGACAGCAGCATGCCTAATCATTCTGTTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCGTCAACTGCAGGGTTGAAACCAAGGTTTAGTGCTTGAGAAC
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCCTTCTCGGGACCACTGGATCTT
GGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCAAGTCAGCAATGC
TTCCAGGGATGTTCATTTTTATCCTGTGTTTTTATCTAGAAAGATTCAAGAGAAT
ATTACAGATTGTTCAAAATGTCCCCTGTTGGATGTTTAAGGTAAACATAGAGAATG
GTGGATAATTACAACTGCACAAAATAAAATTCAAGCTGTGGTGGATGACCAATGTATAAAAA
TGACTCATCAAAATTATCCAATTTAAACTACTAGACAAAAGTATTTAAATCAGTTTTCT
GTTTATGCTATAGGAAACTGTAGATAATAAAGTAAATTATGTATCATATAGATAACTATGTT
TTTCTATGGAAAATAGTCTGTCAAAAATAGTATTGCAGATATTGGGAAAGTATGGTTT
CTCAGGAGTGATATCGTCACCAAAGGAAAGATTTTCTTCTTCAACACGGAGAAGTATATGAA
TGTCTGGAAGGAAACCACTGGCTGTGAATTCTGTACTCGTGTGCCTTGAAACTAGTCC
CCTACCCACCTCGGTAATGAGGCTCCATTACAGAAAGGTGGAAACATAAAGAGAATGAAGGGGGCAGA
ATATCAAAACAGTGAAAAGGGATGATAAGATGTATTTGAAATGAAACTGTTTTCTGTAGAC
TAGCTGGAAGAATTTGGACATAAAAGAATTGAAAGAACACATTTTACCATTTGTGAAA
TTGTTCTGAACTTAAATGTCCAAAACACTTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAAGTTGTTACCTCCACAAATTGAAAAAAAAAAAAAAAAAA
AAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTFVKTVNNFVQRDTFVWWDKLSVNHRRTHLTKLMHTVEQATLRISQSFKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDRYRSLCAF
WNYS PDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSaalgyryygt
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTGCATTTCATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCACTGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAATAAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCAGATGGCAGCTGGTCTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTCACCTTC
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGGAGTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCCGCAGATCCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA
CAAGAAGCCGCCCTGCCTGCCCGGGGAGGGGGCTGGGGCTGGGCCGGAGGCAG
GGTGTGAGTGGGTGTGCGGGGGGGAGGCTTGATGCAATCCCATAAGAAATGCTCGGG
TGTCTGGCACCTACCCGTGGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCGTAGAGCAGGAGCGCTCGTCCAGGATCTAGGGCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGCATCCCGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCAGAGCCCCAGGGAGGTGCCATGCGAGCGGGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCTCTGGCTGGCGTGGCGCCGGCCCCCTCGCCTTCTCGGACGCCGG
CCACGTGCACTACGGCTGGGGCACCCATCCGCCATGCCGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCAGCTGCTCCTGCGATCCGTGCCAGGGCGTGGACTGCCGGGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTGCCGACCGTGGCCATCAAGGG
CGTGCACAGCGTGGTACCTCTGCATGGCGCCAGGCAAGATGCAAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACGCCCTCCGGCTCCCTGAGCAGTGCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTCCACTCTCATTTCTGCCATGCTGCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGCTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAACT
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCCTGGCCCCATTCTGCTCCCTGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACTCCTTGAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTCACTCAACCCATGTGGAAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC
TTCCATCTCCAGCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGCCCT
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTGTTCAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTGCTGTGGAAAGCAGGGGGAGACCTAGAAC
CCTTCCCCAGCACTTGGTTTCCAACATGATATTATGAGTAATTATTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAAATTATATTGATGTAGTAAGTGAGGTTG
TTTGATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTGCTG
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGATGCCGGAAATATCGTGTGAAGTTAGTGCCTTGTCTAC
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAACT
CTGCAATTAAATACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTAAAAATGTGCAGTGGCTACGCCGTAAATCCCAGCACTTGGAGG
CCGGCGGGCGGGATCACGAGGTCAAGGAGTTCAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

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FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
RLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDLNISGIIAAVVVA
LVI
SVCGLGV
CYAQRK
GYFSKET
SFQKS
NSSSKATTM
SENVQWL
TPVIPALW
KAAAGGS
RGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTATTAAACATGCTCCACAGCCGGACCCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACCTCTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA
TTGACAAATGCAAGCATCTTCTTATCAATCAGCTCTATTGAACTTACTGACTGACTG
TGGAACTCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCACTGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA
ACTGCCTGAAAATGTCTGTCGAACACTACAAGAACTCTATAATTAAATCACAACT
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATTCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAACATCAAAGACATGAACTTAAAGCCTTATCA
ATCTTCGAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCTATTAAATAGAA
TACGAAGGGGTGATTTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTTGTGGATAACCTGCCAGATTAAAGAAAATAGAAC
TACTAACAAACCTAGATTGTCTTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCGATTGAGTCTCG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTACCGTTG
GATGAACATGAACAAACACATTGATTGAGCCAGATTCACTGTTGCGTGGACC
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTTCAGGGACATGATGAAATTGTT
CTCCCTCTTATAGCTCTGAGAGCTTCTTCAATCTAAATGAGAAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAACTCTGCCTAATACCCCTGACAGACAAGTTCTATGTCCTATTGAGGAAACACTA
GATATAATGGCGTAACTCCAAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAATAAGAGATATTCAAGGCCATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA
TGTGAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACTGTGATGGTGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCCTGTATAAAATCTCTGGGAAGCAGGAAA
AGAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTAGGTTACCAACAAATATGTCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMLPLRIHVLLGLAITTLVQAVDKVKDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLNSNRQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFIDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSIAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKESMLNSNALSAHYGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVROVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSAAQSARI PSDVKVYNLTHLNPKSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTLLMACLGGLLGIIGVICLISCLSPEMNCDGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTAAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTTGAA
ACTTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQS FVLMILCFHSAS MCPKGCLCSSGGLNVTC SANLKEIPRDL
PPE TVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIAN PWHCDCTLQQVLRSMASN HETAHNVI CKTSVLDEHAGR PFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMV ISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGAACGAAGGCCGCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGC
GGGCTCAGTGCTGTCAGGCTCGGCCACGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGCCCCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACGCATCAAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGGCCGGCG
CCTTCAACAACCTCTCAACCTCCGGACGCTGGTCTCGCAGCAACGCCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCCTCAGCGGCCTAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGTGTCCCACCTGCACGCC
CATCGTCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACGGCCCTACTTGGACACCATGACACCCAA
TGCCTCTACGGCTCAACCTGACGTCCCTGTCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGTCCGCCACCTAGTCTATCTCGCTTCTCAACCTCTCCTACAAACCCATCA
GCACCATGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGCAGCTGGCGTGGTGGAGCCCTATGCCTCCGCGCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCGCTGGCCTGCGACTGTCGGCTCCTGTGGTGTCCGG
CGCCGCTGGCGCTCAACTCAACCGGCAGCAGCCCACGTGCGCCACGCCAGGTTGTCCA
GGCAAGGAGTTCAAGGACTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCCGCG
CCCGCATCCGGACCGCAAGGCCAGCAGGTGTTGGACGAGGGCCACACGGTGCAGTT
GTGTGCCGGCGATGGCGACCCGCCGCCCCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGC
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGGGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGGCCCCATGCCAACAA
GACCTCGCTTCATCTCAACCAGCCGGCAGGGAGAGGCCAACAGCACCGGCCACTG
TGCCTTCCCTCGACATCAAGACCTCATCATGCCACCACTGGCTTCATCTCTTTC
CTGGCGTGTCTCTTCTGCTGGTGTGCTGTTCTCTGGAGCCGGCAAGGGCAACAC
AAAGCACAAACATCGAGATCGAGTATGTCGGAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGCGCCCCGCAAGTTCAACATGAAGATGATAGAGGCCGGGGGGGGCAGGGACCCCG
GGCGGCCGGCAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCCAGTCTCCACCTC
CTCCCTACCTCTACACACGTTCTCTTCTCCCTCCGCCCTCGTCCCTGCTGCCCG
CCAGCCCTCACCACTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGGGGACCCCA
CCTACACAGGGCATGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC
ATAATTCAATAAAAAGTTACGAACCTCTGTAACTTGGTTCAATAATTATGGATTT
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPETRLLLGLKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTQDISENKIVILLYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSIHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLSGNQLTTLEESVFHSVGNNLETLLDSNPLA
CDCRLLWVFRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGCGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCAGCCGCTCGCTCTGCTCCTGCTCCTGC
TGTCGCCTGCTGCTGGCGCCGGGGCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACTCCACGGAGAACCAACCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTGTGAACCAGTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCCGTGAGGGCCAGAACGCTGTTGCTACACTGTGAGGGTCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAACGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCCAG
CAACATGGGAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCCTCCAGCACCTACCAACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTTCCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGGGACACGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATCTAGAGGCGCTGCCACTTCTGC
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTGGGTGCGGTTTGTACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELYSISISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCTTTCTTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCCTGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTCTTGTGTTGCCGCTGGAACAGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTACCATTATTCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTGCTAACCTTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTCTGGGGCTGCAGCTGGTAAAAAGG
CTGCACATCAACAAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTACGAGATATAGACCCGGGGCCTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTT
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGGCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAACAGAACCTTGCTCCTGGACCCCTGCCAACCTTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCTGCCCTGGGGCTGCAGCTGCGACCACATCCAGGGTGGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTTGAAGCCCAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGACTTTGTGGATTACAAGA
ACCTCATTCTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCAGGA
GAAATTCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTCGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTCCTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT
TAGAAAGGATTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACCTC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGGCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCTCACCGTGGGGCATGCTCGTGTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCTTACAAACGAGATGGGCCCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCAAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAACGAAAGGGCCT
GACCCCTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGCCCCCTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAAG
AACTGACAGTGCCTCGCCCTCGGCCCCGGGGCTGTGGGTTGGATGCCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCTGTTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACTTGACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTDVCKEKICSCNEIEGDLHVDCCEKKGFTSLQRFTAQTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPPAPAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSDHIPGSGLKMNCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL
VPGLLLTVFTSAFTVVGMLVFLRNRKRSKRDANSASEINSLQTVCDDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCTGGCAGCGCTCCGCACACATTCTCTGCGGGCTAAGGGAAACTGTTGGC
CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGTCGGTAGGGAGCGAGGGCGAGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCGTTGCCCTGTGCCCTCTGGCAGGCCTCTGGCCCGGGCGGGCGG
CGCGAACACCCCAC TGCGACCGTGCTGGCTCGCCTCGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGGCGCGAGGAGGCCTGCATCCTGCGAGGTGGGCGCTC
AGCACCGTGCGTGCAGGGCGAGCTGCAGCTGTGCTCGCCTCGGGCAGGCCAGG
GCCCGGAGGGGCTCAAAGACCTGCTGTTCTGGTGCAC TGAGCGCAGGCCTCCACT
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCCTGGCTGTCCGACCCCGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGGAGCCCCAACGCTCTGCACCGCGAGATGCGC
GGTACTCCAGGCCACCGTGGGTCGAGCCCGAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCAACGGCTACCTGTCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCGG
GCCGCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTGGGAGG
CTTGCCTGCGAATGTGCTACGGGCTCGAGCTGGGAAGGGAGCGCCGCTTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACCGGGTGCCCACCGCGCCGCCACT
GCAACCAGCCCCGTGCCAGAGAACATGGCCAATCAGGGTCGACGAGAACGCTGGGAGAGAC
ACCACTGTCCTGAACAAGACAATTCACTAATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCACCCCTCAAATGTCCCTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCTCTGCCGTGGTCTTCAATTGTGAGCACAGCAGTAGTGTGTTGGTGTACT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAACGCCCTCTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGATCCTGAGGCCGCTGCTTGGCTC
CAGTTCTGCACATTGCACAAACATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTGCTGGGGAGTCCCTCTGGCTCTAGTGATGCATAGGAAACAGGGGA
CATGGGCACTCTGTGAACAGTTTCACTTTGATGAAACAGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTT
TGGTGTACTGGGGACCGGGTAGTGCCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGATTGAACCTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCAGGGAAAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMVGLVLCFHESPSSQPR
KESMGPPGLESDEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGGCTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCGCGTATC
CCCCGGCTACCTGGGCCCGCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGCGCCCG
GGGGCGCGAACGCCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCCAGAAGGAAAAGTAGTCGTTCTCAATTTCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTTCATGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGCCAGACGGGATTACCCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTCA
TTTATCAGACTTAAGTTAATGCAGATGGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACACATTCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTTGTGTCACAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTG
CACGCCACAGTCTCGATCATCAACACTACAAAGAGGGAAATTGGCGATTCAAGCAGGCGGG
CAAGAACATGAGTGCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCAGAAGAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCTGGATGCCCTAAAAAATAAGCAATG
TTAACAGTGAACGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCT
TGCCCTGCTGTCAGAGGAGCAGCTATGATTGGAAACCTGCCACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTAGAAGTGCATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTTGCCTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMQVGEDGRGKIMPNSFIMMF KTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCGCGGGCTGGGCAGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTCTCCCCGCTCAGCCCCATCCGTGTACATACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACCTGGAG
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
TAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGTCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGAGTGACAGAGGGAGCCAAGT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCCAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGAGACAGAGGTGTGTCCGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCACTGGTGGTCAACGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGCGCAGTGACCGTGTGCTGGAGGGCTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGGGTAAGCACCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGGAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTTCAACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTACCATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPPPKGVLPAVLWGLSLFLNLPPIWLQPSPPPQSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSDKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCGGTERPCGGYGCCEGEGETRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVC SACFGPCARCSGPEESNLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKCNCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCGGAGCTGCAGCTCAAAGAGGT
GCCCACCTGGACAGGGCGACATGGAGGAGCTGGTCACTCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCGCGCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGCAGCACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCAGAAGTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGCACCTGCCGGCAGCCCCCGAGGCCCTGGCCTTAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAAGGAGGCTCCAGCCATGGCCCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGAGGGTACCAAGGAGAGCTG
GCGATGACTGAACGTGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTTACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCTCCACCACCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLQSVSQREHLGPLASGAHKLVRFASQGAPAGLGEHQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGC~~GG~~CTGTTGTCAAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTTCATGAGGACCGGG
TGACCTTCTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT
GGGATAGTGATGCCAACGAATCCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAAGCCTCTGATAACTGGAGAAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGATGGAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCTGATTCTCCTGGGAAT
CTTGGTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAACCAAACAG
ACCTCGTCATTCC~~TGGTGTG~~AGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC
TACACCCACAGGGCCCCCTACTTCTGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAAATAGGTATCTTGAGCTGGTTCTGGCTCTTCTGTACTGAC
GACCAGGGCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCCTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGATCCCTCTGCCCTGTCCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTGTTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAAACTGGAGGCTGGCGCAGTGGCTACGCC
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCCACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVIEW
KFDQGDTTRLVCYNNKITASYEDRVTLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTSEQDGSPPEYTWFKDGIIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCCGCGAGCCCGCTTCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCCAACCAAGTTCCAGTGCCGACCAAGTGGCTTATGCGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGTGCACGGCCA
CCCAGACTGTCCCAGCTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACCTGCCTATGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTTGTCCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCCTTGAGGACAAGCAACTGCCACCCGTCACTCACGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGTACCCGGGACACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPTLESPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCCGGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGCACAGATGCC
GTTAGACTGGGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTTAGCTGGCCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGTGCTGACCCCGCATTCCCAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTTCAATTATGTCGCGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTGTGAGC
TCCAGACCTCCTTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTCGTATCTTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCAAATGGTAGTCACGGAGATTCGTCT
GCCACCCGGCCCTGTGAGCGCTACAACCACCGAACTGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCGGAG
TTCCAGCAGTGACCTGACTTGTGGTAGACGGCGTGCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGGGCTTGAGTGCCTTAGGCCCCGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTAACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTCGGACAACCTGACATA
ATTGCCAGCAGGAGGGAGGTGGCATCCACCAAGCCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTAAAAAATTCCCAAAGTGTCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTTCTCTTGAGTAAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLGATKRLCLKHFNGLGWI PSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMSLCRDDGTWNNLPLICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTS DYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLLVLARMFQT KFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYM ASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDI IIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGC~~CC~~CTCCCCCGCCTCCCGTGC~~GG~~TCCGTGGCTAGAGA
TGCTGCTGCCGCGTTGCAGTTGTCGCGCACGCC~~T~~CTGCCGCCAGCCGCTCCACC~~G~~CGT
AGCGCCGAGTGT~~C~~GGGGCGCACCCGAGTCGGCCATGAGGCCGGAAACCGCGCTACAGG
CCGTGCTGCCGTGCTGGTGGGCTGCCGCCGACGGGTCGC~~T~~GAGT~~G~~CC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGC~~T~~TTGTTA
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAAC~~TT~~GAGGAAGCCAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGAC~~TT~~TATGCTGGACTGATGGCAGCATAT
CACAATTAGGAACTGGTATGTGGATGAGCCGCTGCCGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGAGGCCCTACATGTTCCAGT~~G~~GAATGATGA
CCGGTGCAACATGAAGAACATTCAATTGCAAATATTCTGATGAGAAACCAGCAGTTCC~~T~~
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACAC~~CT~~GTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAAGCTGCC~~T~~GAATCTGGC~~T~~ACAT
CTTAATCCCCAGCATTCCCCTCTCCTCCTGTGGT~~C~~ACCACAGTTGATGTTGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCC~~T~~AGCACAAAGAAGCAACACACC~~A~~
TGGCCCTCTCCTCACCAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCAATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGT~~G~~AGCGTGGAGAGTGGATTGACCAATGACATTATGA
GTTCTCCCCAGACAAATGGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAA~~AA~~ACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGT~~C~~TGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTGGTTGGTTGTATCTAAC~~TT~~TAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGCTGTGGAGCTGGAAAACCACCTCTGTTTCC~~T~~GCTATACAG
CAGCACATATTATCATA~~C~~AGACAGAAAATCCAGAATCTTCAAAGCCCACATATGGTAGC~~A~~CAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKTFKESREAALNAYILIPSIPLLLL
VTTVVCVWWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFVTLVSVESGFVTNDIYEFS
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAACAGACTTGT
GTTTGCCTCCTGCAGCCTAACCCGGAGGGCAGCGAGGGCCTACCACCAATGATACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTGACACACGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATCCCTTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGTCTGTATCCAACACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCGGACAAGATCAGAAAGCTGTATCTATGCCGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAAGTGCCTTATAACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHLNPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LDMLNAMS VYTLSPEKYHALCSQTQVM EVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAAACAAATATTGCTGCTGGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACC GTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGT CCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGAGGGTGTCA GGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGGCTTGGGGAAAGAACACCTGCAACC ATGATGAAGACACGTGGT CG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTGTGATGACA ACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGAAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGGTTGGCCGATCTGGCTGGATAATGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGC CAGCACAGATTTGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGGACTTATACTTGGTGC CCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGA ACTACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCC CAGCCTCCATAATTGTGTGTAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCA TTGTCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATT TAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAAC TTTATTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGLASPGVRLVGGHLRCEGRVEEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCCGCGACCGCGTGGCGGACCGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG
CGTCTTCGGCCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCAACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCCAGGCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTCAGCCTCATGGCCTCCAGGGCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACGACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAGGGCGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCAATTGTTATTGCAGCTTATAATGGTTAC

TOP SECRET - EYES ONLY

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKEAKVFYAAGA
KLVLICRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCAGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAUTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGTGCCAGGTTACACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCAGTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACGGCTGCCTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTAACACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAGCACCTAGTTCTGAAAACGTGATTTACCAAGGTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTCAATA
TCATTGGAGGCTTGGCAGTCTCATTACTACCACCTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAAGAAAATGAAGAAAAGAA
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTCACCTGAAAGGCTTGC
AATTGTACCATACCGTTATTAAACATATATTATTATTGATTGACTTAAATTGTT
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACCTCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGATAACCTCACATTCAATGCCAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGATT
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCCGGACCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCCTGAGAGATGGTGGTGCCATGTGGAAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCCTGGCCCTGTGATGGCTGTTCGCTCCCTATA
CAGAAGTGTTC
GTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAACGATGCCAGTAGTTCTGGCTACAGGGTGGGCCGG
AGGTTCATCCATGTTGGACTCTTGGAACATGGCCCTATGTTGTACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATAACCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCAGATAATTCCCTGAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGGCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAAATTCTGTACCAAATTGGCT
TGTGGATGAGAACGAAAAAGTACTCCAGAAGCAGTGCCTGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGCTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTAAGGAAATTGGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGTAAGGAACTATAGTTGAAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAAGTGAATCATGAATAATTAAAGGTTCTGA
TCTACAATGGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTGTACATGATTAATCGA
TTCATTTATGGAAAAGGATGGATCCTTATGTTGATAAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATGTAAGGAAACAGAAAATGTCATAGGAATA
TTATCTTTCATATCTGCAAGATTTTTCATCAATAAAATTATCCTGAAACAAGTGAGC
TTTGTGTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAAATGA
AATTTAGGGTCTTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTTSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAAALTERSLMGMDWKGSQEYKKAEKVVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCCGGCTCCGAATGGCACATGTGGATCCCAGTCTTGGCTACAACAT
TTTCCTTCTTAACAAGTTCTAACAGCTGTTCAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTT
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCCTAACAAAGCTTCAAAAAACAGGAGGCACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAAGACTGGTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTTAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGGTC
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTGGTCTGACCACTCTGCCTGTGTTT
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTCTCAGTGGTCTGGGTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTTCAAGGACCTTCACTCTGAGAAATCGTGAUTGGACCTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCCAGAAGAGGACAACAAGTCTCGTACCCG
CCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCTGTGGAGCCTTACCCAGGGGTCTGCA
AGCTGCTGGGCTGGATGACCTCTCATCTGGTGGAGCCATCCCACAAAGAAGGAGCACTAC
CTGTCAGTGTCAACAAGACAGGGCACCAGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCCTGAGGGTGTGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGCG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCTGCCCTGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGCCAACCTGGGACTCACTGGCCC
AGGCCTTCAATATCACCAAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG
CAGTATCACCAACCGCCCGATGACTCTGCCCTGTGTGCCCTTCCATCCGGGCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTAGCTATTGGTGGAGATTTA
ATTACACCTCTCAGCAAAGAGTCCCTTTGGAAGGTAAGGAGCTATTGGTGGAGATTTA
GCAACTTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGTTAATTTG
ACTTAGCTTCTAGCTACTCCTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTGHQGTGAVYVGAINRV
YKLGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSL
YQGVCKLLRLDDLFIΛVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKI PSDLALVSHFDIFYIYGFA SGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFH SYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEQN
LELNWLLGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFGTKSGKLKKVRVYEFRCSNAIHLLSKE SLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCCTCCCGCCGCGGGCTGAGTGGACTGGAGTGGAAACCCGGGTCCCCCGCCTTAGAGAACACCGCATGACCA
CGTGGAGCCTCCGGCGAGGCCGGCCCGCACGCTGGGAACCTCCCTGCTGGTCCTGGGCTTCCTGGTCTCC
GCAGGCTGGACTGGAGCACCCCTGGATCTGGACTTCGGGGCTCCACTATTCGTGTGCCAGGGAGTACT
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGCTCCACTATTCGTGTGCCAGGGAGTACT
GGAGGGACCCCTGCTGAAGATGAAGGCTGTTGAACACCCTCACCAACCTATGTTCCGTGAAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTGGAAACCTGGACCTGGAGGCTTCGATGGCCAGAGATCG
GGCTGTGGGTGATTCTGCTCCAGGGCTACATCTGCACTGAGATGGACCTGGGGCTTGCCCAGCTGGTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTCACCGAAGCAGTGGACCTTATTTGACCAC
TGATGTCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATGGCTGCAAGGTGGAGAATGAATATG
GTTCTATAATAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGGAACTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCACT
CAACACACGAGCTGCAGCTACTGACCACCTTCTTCACGTCCAGGGACTCAGCCCAAGATGGTGTGGAGT
ACTGGACGGGTGGTTGACTCGTGGGGAGGGCCTCACAAATATCTGGATTCTCTGAGGTTTAAAACCGTGT
CTGCCATTGTGGACGCCGCTCCATCAACCTCTACATGTTCCACGGAGGACCCAACCTTGGCTCATGAATG
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAACCGCG
ATTACACGCCAAGTACATGAAGCTCGAGACTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTCTTCCCAAGATGCCGTATGAGCCCTAACGCCAGTCTTGTACCTGTCCTGTGGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCC
TCGGGTACATTCTCATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCTGATCGGGGCAGG
TGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGATCGTGGCGAGTCAACTATGGGAGAATATTGATGACCAAGCGCAAAG
GCTTAATTGGAAATCTCATCTGAATGATTCAACCTGAAAACACTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGGCCCTGGACAAATGGNNTCCCTCCAGAAAACACCACATTACCTGCTTTCTTGG
GTAGCTTGTCCATCAGCTCACGCCCTTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGTTGTATTCA
CTAACGGCCAGAACCTGGACGTTACTGGAACATTGGACCCCAGAAGACGCTTACCTCCAGGTCCCTGGTGA
GCAGCGGAATCAACCAGGTATCGTTTTGAGGAGACGATGGGGGCCCTGCAATTACAGTTCACGGAAACCCCC
ACCTGGCAGGAACCAAGTACATTAAGTGAGGGTGGCACCCCCCTCTGCTGGTGCAGTGGAGACTGCCGCTC
CTCTTGACCTGAAGCCTGGCTGCTGCCCCACCCCTCACTGC~~AAAAGC~~ATCCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCTAAGCCTGCAGGAAAGGTGGATGGCTCTGGGCC
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTCTGTGCCAGGCTGTGGCTGTCTCTAGGGTGGAGC
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAGTGTGAAACAGTGCCTTGCACTGGGACGTACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGCTTTGCTGGTTCTGGAGGCTTGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAATCCTGGGTGTGTCACCAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCCTCACAAACCTCTGAGCCTCTTGGATTCTGGAAGGAACCTGGCTGAGAAACATGTGACTTCCCC
TCCCTCCCACTCGCTGCTTCCCACAGGGTACAGGCTGGCTGGAGAACAGAAATCTCACCCCTGCGTCTCC
CAAGTTAGCAGGTGTCCTGGTGTTCAGTGAGGAGGACATGTGAGTCCTGGCAGAACCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACCCATGGCCATGTCTGCA
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGGCCATGGCCATGTCTGCA
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGGCCATGGCCATGTCTGCA
ACAGAACGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGCAGAGCAGCCCTCCTTC
GAAGTGTGTCAGTCCGATTTGAGCCTTGTCTGGGGCCAGCCAAACACTGGCTTGGCTACTGTCC
GTTGCAGTAAAGCTATAACCTGAATCACAA

TOP TWO - 523 524 525 526 527

FIGURE 64

MTTWSLRRR PARTLGLLLL VVVLGFLV LRR LDWSTLVPLRLRH RQL GLQAK GWN FMLED STFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSNDKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLNVQGTQPKMVM EYWTGFDSWGGPHNILDSS EVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVT SYDYDAVLTEAGDYTA KYMKLRDFFGSISGIP
LPPPPDLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKP INMENLPVN GNGQSF GYI LY
TSITSSGILSGHVHD RGQVFVNTVSIGFLDYKTTKIAVPLI QGYTVL RILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSPLKNFRIYS LDMKK SFFQRFGLDKWXSLPETPTLPAFFLGSL SIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLS SGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTAGGGTGGACGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCGGCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCC
AAGAAGCTGCTCTGCCCTCGTCCCTGCTGCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCGTAGTGGATAGGGCATGACCGGTTCTCTAGACGGGCCC
CGTCGCTATGTTCTGGCAGCCTGCACTACTTCGGTACCGCGGTGCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCTCAAGCCATACAGTTATGTCGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGGTCTCCCATCCTGGTGTGCTGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTGCTGCCCAAGATATATC
CATGGCTTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTCAGCTACATGAGGCACTTGGCTGGCTCTCGTGCAGTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTGGCCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCAGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCCTCCGATTACTACAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTGCTTGGCCCCGTGGGCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAAATATTGGACGGGAAACTGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTGGCTAACAGCAGTGACTCAAGGGCTGTTGAAGCCACCAATTCTG
GGCAAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACATTGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGTTCCCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACTTGAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCGTCTCCACTAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACCTCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTAACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNISIQVENE
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPhGPLVNSEYYTGWLWQNHSTRSAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFAIRDVISKFQEVPPLGPLPPSPKMM
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQQPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTTCTGGTTATTCAAGGATACCTTGAAAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT
GCGTTCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGTGCCCAGTGCTGTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTCAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTCTAACATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACTGGAT
TTAAAGTCCAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATTAAAAGCAGT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCTAACAAACAAGCTCGAACCTTACCAAGTGGAGTATT
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGGCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG
TGGAAAGATCACCTTTGATAACCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAATGGGATTTAAACTAAGATAATATGCAAGTGTGAGGAAAC
AACTTCCTAGATTGCAAGTGCACGTACAAGTTATTACAAGATAATGCATTTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGGTTAAGTCATTCAAAATCATTGTTTTCTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRLQHISRNAQDKQELHLFMLSG
VPDAVFDLTLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPA WVYLLKNLRELYLIGNLNSENNKMIGLES LREL RHLKILHVKSNLTKVPSN
ITDVAPHLT KLV IHNDGT KLL VLNSL KKMMN VAELE LQNCELERI P HAIF SLS NLQ ELD LKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTI PPS ITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITS LP
EKVGQLSQLTQLELKGNCLDR LPAQLGQCRMLKKSGL VVEDHLFD TLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCCACCGCGTCCGGGCTTCTCTGGACTTTGCATTCCATTCTTCACTGACAAACTGACTTTTTTATTC
TTTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTTCTTCTCCTCCCCCTGACATTGGCATGCTTAGTGTTGTGGGAGGGAGACCACGTGG
GCTCAGTGTTGCACTTATCTGCTTAGGTACATCGAAGTCTTGCACCTACAGTATTGCTGTC
ATCGCTGGTGGTATCCTGGGGCCTGCTCTGCTGATAGTTGCTGCTCTGTCTTACTTCAAAATACACAAAC
GCGCTAAAAGCTGAAAGAACCTGAAGCTGTGGCTGAAAAAAATACAACCCAGACAAGGTGTGGTGGCCAAG
AACAGCCAGGCCAAACATTGCCACGGAGCTTGTCTGCCCTGCACTGCTGTGAAGGATATAGAAATGTGTGCC
AGTTTTGATTCCCTGCCACCTTGCTGCGACATAATGAGGGCCTTGAGTTAGGAAAGGCTCCCTCTCAA
GCAGAGGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTCAGGCACAGAAGAAGGCACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCTGGAACAGCTGCTGGAGATCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCCAGGAAGGAGTTGGGAGAGAGAACCCCTCACTGTGGGAATGCTGATAAAACAGTCA
CACAGCTGCTTATTCACACAAATCTACCCCTGCTGGCTGGAACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCTATAAAAGCTGTCGCTCTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTGTA
AGAAGGGCTCATGCCATTGCCCTCTTAAATTCTCTCTGTTGGGGAGCTGACAATGGCGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCTAGGGGGTGCCTAATGGCAGAGACCCAAAGCCATGATCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAAGACAGAAAACAAAGCATGAGATTATCTTCTTCTATGTCAGCTT
GATCCAGATGGAAAGCTGTGAAAGTAAAAACATTAAAGTCTTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG
CAAGCTGCACTAAAGAAGCTATGTTCTGATTGAAATCATCATCCAGTACATTGACGTTCAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCCTTGTCTTACTACTTCTCTCCTAACATCTCTTCTAACACTG
GGCGGTTACCTGGATACCTGGAGGATCCTTACCCAGCCCAATTACCCAAAGCCGATCTGAGCTGGCTTAT
TGTGTGTCGACATACAAGTGGAGAAAAGATTACAAGATAAAACTAACTTCAAGAGATTTCCTAGAAAATAGAC
AAACAGTGCAAATTGATTCTTGCCTCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCCACCTTCGAATCGTCAAACTCTGACTGTCGTTGTCTACAGATTATGCCAATTCT
TACCGGGATTCTGCTTCTACACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACTTGCTCTCT
GACAGGATGAGAGTTATTATAAGCAAACCTACCTAGAGGTTTAACTCTAATGGGATAACTTGCAACTAAA
GACCCAACTTGCAAGACAAAATTATCAAATGTTGGAATTCTGCTCCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCATTACTACACCAATATAATCACCTTTCTGCATCTCAACTCTGAAGTGTAC
CGTCAGAAACAACCTCCAGATTATGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATATAACCCAGCATGGCTTTTGAACTTCAATTCA
TTGAAAAGACTATACTTGAATCACCATATTATGTGGATTGAAACCAACTCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAATTGGGGTGTCTCTGATACCTGAGAGGCCCTCCACCTGACTTGCATCTCCAAACC
TACGACCTAATCAAGAGTGGATGTTGAGATGAAACTTGTAAAGGTGATACCTTATTTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTGAGAAGTGTGAGCTGTGTTATCTGAGTGTAAAGTTGATATGTGAT
AGCAGTGACCAACAGTCTCGCTGCAATCAAGGGTGTCTCCAGAAGCAACAGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAGGGATCGAAGTGCAGTGGCAATTCTAGGATTCTAGCAT
GAAACACATGCGGAAGAAAACCTCAAACCCAGCCTTCAACAGTGTGCATCTGTTCTCATGGTTCTAGCTGT
AATGTGGTGAAGTGTAGCGACAATCACAGTGAGGCAATTGTAATCAACGGGAGACTACAAATACAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCCCTAAGTGAGACATGTTCTCAGGATGCCAAAGGAAATGTCACCTCGT
GGCTACACATATTATGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCCTGCATGTA

FIGURE 70

MELVRRLMPLTLLLILSCLAEILTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSQLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSVYL
QCKVLICDSSDHQSRCRNQGCVSRSKRDIISSYKWKTDIIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGAGCCTGCAGAGAGGGACAGCCGGCTGCGCCG
GGACATGCGGCCCAAGGAGCTCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGGCCACGCCGCTCGACCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCCTCGTCCCAGCTCGGTAGCGAGTGGTCTGGTGTATTGGAAAAGGAAA
AGATACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACATTACAGAAAATTAAATGCCAACAGTGGCAGATATTTCAGGC
CTCTGGTGCCAAATACATTGCTTAACCTCCAAACATCATGAAGGCTTACCTTGTGGGGT
CAGAATATTGCGGAACGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCCTTGGACTGTACTATTCCCTTTGA
ATGGTTTCACTCGCTCTCCTGAGGATGAATCCAGTCATTCCATAAGCGGAATTCCAG
TTTCTAAGACATTGCCAGAGCTCATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGGCCAGTTGGGGCACAGTAGTCACCAATGATCGTGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATTTGCCA
CATAATGGAAAACGATGCAATGACAATAGACAAACTGTCCTGGGCTATAGGAGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTAGAACAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTTCTAAATGGGCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC TG
GATTCTTGGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACGGATAAGAAAATTATTGGCAGTTCAAGCCCTTCCCTTTCCACTA
AATTTTCTTAAATTACCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAACCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATAACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATCTGTAACGGTGCACCTGTATAGGGCACTTACCAAGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCAATTATAAAACATAAGTGTACTGTAACTTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGWSWLKVNGEAIYETY
WRSQNDTVTPDVWYTSPKKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCTGGCCAAGGCTCTTGCGTGAGAAGAGCT
TTCCATCCAGGTGTCACTGCAGAATTATGGGATCACCCCTGTGAGCAAAAAGGCGAACAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGCACTATGGCTGGGTTGGAGA
TGGATTCTGGTCATCTCTAGGATTAGCCCCAACCCCAAGTGTGGGAAAATGGGTTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACTCATCTGAT
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCACCAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCACTGACAGTACCTACTCGTGGCATCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCTGCTCCAGCTTCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGAAACTAGCACCATGTCTACAGAAAC
TGAACCATTGTTGAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGCTTGATTTGC
TATGTCAAAAGGTATGTGAAGGCCTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAGAACCAAAGAAGAAAGTCCACCCCTT
GGTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGACCAAGAGAATGC
CCTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCTACCTCCAAAGCTCCACGGCC
TTCTAGCCTGGCTATGCTTAATAATATCCCACGGAGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG
TGGTTGAAAGCCAAGGAGTCAGTGGACCAAGGCTTCTACTGATTCCGCAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTCTGAGCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTGAAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT
AGGAAATATACTTTACAAGTAACAAAAATAAAACTCTTATAAATTCTATTCTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTCTTCA
GTTTGATATTCTAGCTTACTCTTCAACTAACTTAAATTATTAAACATACCTAACAGAAG
ATTCAATTGTTACCTCTATACCAAAAGCACATTAAAAGTGCCTTAACAAATGTATCACTA
GCCCTCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNSPKCGKNGVGVLIWKPVSQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASFKNNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGCGGGTCTGGCACCTCTAATTGCTCTCGTGTATTGGTGCCTCGACTTCACGATGG
CTCGCCCAACCTTATACTACCTTCTGCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCAACCCAACCGAAGACGGTAACCCGTGTACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCCCTAAATACAAC
GTACAGGGCTAAATTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGGCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGGCTCAACCCCCACCACAGTGTCA
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGGCCAACTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTTGGTCAGTGTGTTAACTGCTTATC
AGCTATTCAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTAACCCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCCCCAAGGACTCTTGCTCCCTTAAGCCCTCTGGCTTGTGTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTCGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTATCATTGAAGACAATATTGAACAACCCCTATTGTGGGATTGAGAAGGGTGAA
TAGAGGCTTGAGACTTCCTTGTGGTAGGACTGGAGGAGAAATCCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNI PEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTGAGGAGCTGCCCTGGGACGTTGCCCTG
GGGCCAGCCTGGCCGGTCACCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCA
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGGCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGG
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTTCTTACCAAGTCCCCA
ACGGGCGTACCAACTTCCACGAGGGCCAGCAGGTCTGTGCGAGAGCAGGCTGCCGTG
GTGGCCTCCTTGAGCAGCTCTCCGGGCTGGAGGAGGGCCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCATCATGTTGCCCGGCAGCCCTGCCGTGG
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGGAC
AGCTTTGCCGCTGGAAGTCCATGCCCTGGACCGCTGCCACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCGTGGTCACCCGCATCCTAAGTGGGCCCCAGAGCCTGGG
CCGAAGCTTGCGCTCCCCGACCCGCAGAGCCGCTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGATTCCACTGGCTGTATTTATTGAGTGGTT
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGTAAGCAAACAGAACCCATGCCCTCCCTGCTCCTG
GATGCCCACTCCAGGAATCATGCTGCCCTGGGCCATTGCCGTTGGCTCTG
GAGGGTCCCCGCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGGCCAGAGTGGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTCTCCCTGCC
CAGCCTGGGGAAAGAAGAGGGCCTGGGCCCTCCGGAGCTGGCTTGCCCTCCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTCCAGGCAGAAATCTGAGGAAAGAAACTCCCCTCCCCGTTCC
TCCCTCTCGGTTCCAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCCTCCGCCAA
AA
AA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGACCGATGATGTGGCGACCCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGTGGATCGCGCACACGCAGCAGCGGA
CATACGGGACTCGGTGAGCGCGGCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCGCCCGTGAAGAATTGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGGCGTTCCGGTGGC
CGACCCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG
AGTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGGGATCTGACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGGTGGAGGACTGGGTGCTGCCCTGCCAGGACCAGCCC
CTGGTGGAAGCCAACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
ACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCAGGAG
GCAGATGCAGTCCCAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTACACCCCCAACCCCAAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCCTGGCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

0 9 8 7 6 5 4 3 2 1 0 2 4 4 6 7

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRILSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCAGGGCGCGGGTGCAGGGGATCCCTGACGCCCTGTCCCTGTTCTTGTCGCTCCCAG
CCTGTCTGTCGTCTTGGCGCCCCGCTCCCCGCGGTGCGGGGTTGCACACCGATCTG
GGCTTCGCTCGATTGCGCCGAGGGCCTCCCAGACCTAGAGGGCGCTGGCTGGAGCAG
CGGGTCGTCTGTCTCTCCTCTGCAGCCGCCCCGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCGGGGCTCCCGCACCCCTGGCCTGCCATTCTCCCTCTCCAG
GTGTGAGCAGCCTATCAGTCAACCATGTCCGCAAGCCTGGATCCCGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGCCCTCCATTGCTATCACATG
TTTACCAAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTCTGTATCGAGCATATGTGG
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCTACC
TGGTCGAGAAAATATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTAGAT
GGTCTGCTCTTCAAGTAACTAAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACAGACTAAAGAAAACACCCGAGAAGAAAATGG
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTAACTTGAA
AAACTTTACATCAGCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGATCCCCAAAGTGGTGGTGGTATTGATGGTGGCCTTGTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACCTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTCTTACACATGCCAACTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAACGCTGTGCACTCATGAACAAATGATGTGAGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCCTC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGGCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGCTTAGCTGTATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTCCCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCAGGCTGCAAGCTGCTG
CACATGATGCGAGGAATCACTATCTCTCTGTTGGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAACTGAAAGAAAAGTACAAGGGATCCAGTGTAAATTGTATT
CTCATAACTGAAATGCTTAGCATACTAGAATCAGATAAAAATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

TOP SECRET

FIGURE 82

MSAAWIPALGLVCLLLPGPAGSEAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSTQEATGQAVSTAHPPTGKRLKKTPPEKKTGNKDCCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCGCACCGCGGCCACCGCGCCATCTGCACCCGCAGCCC
GGCGGCCTCCGGCGGGAGCAGCAGATCCAGTCCGGCCCGAGCGCAACTCGGTCCAGTCG
GGCGCGGGCTGCGGGCGCAGAGCGGAGATGAGCGGGCTGGGCCACCCCTGCTGTGCCTGC
TGCTGGCGGGCGGGTCCCCACGGCCCCCGCGCCGCTCGACGGCGACCTCGGCTCCAGTC
AAGCCGGCCCGGCTCTCAGCTACCCGAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTGAGGAACGTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
CAGAAGAACGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTAT
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTAACGCCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGTGGAGACAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCCTGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCGACCTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTCATGGAGGAGGTGCCAGGGACTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCT
GCACTGCTGGAGGGGAAGAGATTTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTACA
TCTTCTCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTGCAATTGTTCA
TCCCCCAGGCTGTCTCCAGGCTTCACAGTCTGGTGTGCTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTGTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCTTCAAGCTGTTGAGATGAAATGTTCTGTTCAACCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTATTGTTCTCCTCGCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCT
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCACACCAGCCTGGGCCACCAA
AAGTGCTCCCCAAAGGAAGGAGAATGGATTTCAGGCACTGCACATCTGGAATTAAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAACACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGAGCCGTCTTAATGAAGACAATGATATTGACACTGTCCTCTGGCAGT
TGCATTAGTAACTTGAAAGGTATATGACTGAGCGTAGCATACTGGTAAACCTGCAGAAACA
GTACTTAGTAATTGAGGGCAGGATTATAATGAAATTGCAAACACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCGACTGCCAACACTGAACACTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGACAGTTCTTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCAATTAGAAATCAAGC
ATAAAACTCAACTGCAAAAAAAAAAAAAAA

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FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCQFQRLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASCGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVROELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTTCCTCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGCAGGGCTGGCCATTACCTCTGCAGCTCCTTGGCTTGAGTCAGAAAACATGGGAGGG
CCAGGCACGGTGAECTCACACCTGTAATCCCAGCATTGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG
TTCGAGACCAGGCCAACATGGAGAAACCCCCATCTACTAAAATACAAAATTAGCCAGGAGTGTTGGC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT
CAGCTGAGTGACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
GGGGTAGATACTGCTTCTGCAACCTCCTTAACCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCGCTG
GCAATGACTGAGCAGGCCAGGCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCG
GTGAGAATGACTGCCCTGGGAGGGTGGTCTTGGGAGGCTGGCAGGGTTGCTGACCCCTTACCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCCTGAGCTCCACCAATGAGGCTCTCGTGGCCCC
ACTCTGCTAGCTTGGGTTGGCTGGCCACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCCCTCTCA
GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCTACCGCGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCCCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGCTCCTGAGAGCAACAGCATTGT
CCGTTGAGGACAGAGTGAAGCTGGCTACCTGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTGG
TGCCCGAGACTGTGATTCCATGCCCTGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAACAGCTGACCCGCT
GGAGGACACAGCTTGCAGGGCTGGCCAGGCTACAGGAACCTATCTCAACCACAACCAGCTACCGCATCGC
CCCCAGGGCTTTCTGGGCTCAGCAACTTGTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCCATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGCGTAGCCTGGTCTAGCAGGCTAGAACCTGCGGGAGATCTCCGACTATGC
GAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGCTAGAACCTGCGGGAGATCTCCGACTATGC
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTATGACAACAGCTGCCCTGGGCTGCCAGGGGCAACT
GGAACAGGTGCCGGCTCAAGTTCTAGACCTCAACAAAGAACCCGCTCCAGGGTAGGGCCGGGACTTTGC
CAACATGCTGACCTTAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCATGACAAGTTGCCCTGG
GAACCTCCCCGAGCTGACCAAGCTGGGACATCACCAATAACCCACGGCTGTCTCATCCACCCCGCCTTCCA
CCACCTGCCCTGGGAGATGGGACCCCTCATGCTCAACAACACGCTCTAGTGCCTTGACCCAGCAGACGGTGGAGTC
CCTGCCCAACCTGCAGGGAGTAGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCATCGCTGGGCAATGC
CACGGGCACCCGTGTCGCTTCATCGAGCCGAATCCACCCCTGTGCGGAGGCTCCGGACCTCCAGCGCTCCC
GGTCCGTGAGGTGCCCTCCGGGAGATGACGGACACTGTTGCCCTCATCTCCCCACGAAGCTCCCCCAAG
CCTCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGACTGGCGAACCCGAACCGAGATCTACTG
GGTCACTCCAGCTGGCTCGACTGACACCTGCCATGCAGGCAGGAGGTACGGGTGACCCCGAGGGGACCC
GGAGCTGCGGAGGGTGACAGCAGAACAGGGCAGGGCTATACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTGTGGCCGTCTCCTCCAGCCAGGAGGGAGAAGGACAGGGCTGGAGCTCCG
GGTCACTCCAGCTGGCTCGACTGACACCTGCCATGCAGGCAGGAGGTACGGGTGACCCCGAGGGGACCC
CTGGTCCAGTGCCCTCTCCCTGCCGGGAGGGCCACAGCTCTGGCCGCTGCCTGGGAACCCACAGCTA
CAACATTACCCGCTCTCAGGCCACGGAGTACTGGGCTGCTGCAGTGGCCCTTGCTGATGCCACACCA
GTTGGCTTGTGTATGGGCCAGGACCAAGAGGGCAGTCTTGTGCAAGTGGCCCTTGCTGATGCCACACCA
TGCCATCCTGGCTCTGCTGTCTTCTCCCTGCCAGCTGGGCTTCTGGGCTGGAGTGCCAGATCCTCAGAAGGGAGACACTGTT
GGTGTGGGTGGAGGCGGCCCTCCAGCCTGGGTTCTGGGCTGGAGTGCCAGATCCTCAGAAGGGAGACACTGTT
GTCTGCTCTCCCTCGTCTGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTT
ACCATTGTCTAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTACAAA
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGC
CAAGACAGATGGGCTTTGTGGCCCTGGGGTGCTCTGCAGCCTGAAAAAGTGGCCCTTACCTCCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCCTCCCCATCTT
CTCTGCCCAGGGCTCTGGGCCCTGGCTGTCTTCTGCTGCCCTACCTGTGCTCCCGGGCTGCACCCCTTCTCTTC
TCTTCTCTGTACAGTCTCAGTTGCTTGTGCTCTGCCAGGGCTGAAGGGAGGCCACTCCATCTCAC
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGAATTGTACCTTGTGGAGAA
ATGTGTCACCTCCCCAACCCGATTCACTCTTCTCTGTTGAAAAATAAAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATAVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGALKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHLPQMELTMLNNNALSAHQQTVESLPNLQEVLHGPNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGDADTKTVVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEWACLAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGGCGCTGTTGAGAAGGTGAAGAACGTTCCGGACCCATGTGGAGGGAGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCTGCTACACCCTACTACGTGCACAA
CATCAAGTTCGACGCTGGACTGCACCGTGGACATTGAGAGCCTGACCGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCGCTCTTACATCAGCTAGTCATCTTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTAGGGAGAGCAGCTACAG
CGACATCCCCGACGCTAAAGAACGACTTCGCGCTTACATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGCTTCTCGGGAGGTGAGTGAGAACAAAGCTGCGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACCGCAGGACAAGCTGGAGCTGACCTGTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGAGGTGACCATCCCCG
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTTGAGCTACCCACAGCGCCAAGATTGAAGCGCTGCC
GGCCTTCTCGCGAGAACCTGCGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGCGAGAACAAACCGCTACATGTCATCGA
CGGGCTGCGGGAGCTCAAACGCCCAAGGTGCTGCCGCTCAAGAGAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGACCAAGCTCATGTCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTCCAGCACCT
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATGCCTACATCCCCATCCAGATCGCAACCTCACCAA
CCTGGAGCGCCTCACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTACTGCGCGAAGCTGCG
CTACCTGGACCTCAGGCCAACAAACCTGACCTTCCCTCCGCGACATCGCCTCTGCAGAACCTCCAGAACCT
AGCCATCACGGCAACCGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCAGGAGCTGAGCTGGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCGGG
CAACCGGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAG
GCCGCCAGCAGCAAGCAGCAGGCCAGCGCTGGGCTGGGAGGAGCTGGGGCCAGGCCAGCTGGGGCTGAGCTCC
AACTCCGGACAGCCAGGACAGCCTCGCGCTGGGAGGAGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGGGGCTGGCCCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGTGTTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCTCCCTGGAGGGCAGCTCTGCCCAAGGGCTGAG
CTGCCACCAGAGGTCTGGGACCTCACTTTAGTTCTGGTATTATTTCTCCATCTCCACCTCCTCATCC
AGATAACTTACATTCCAAGAAAGTTCAAGGCCAGATGGAAGGGTGTTCAGGAAAGGGCTGCCCTTCCCC
TTGTCTTATTAGCGATGCCGCCGGCATTAAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGCAACCAG
CCATGGGACGGTCACCCAGCAGTGCCTGGCTCTGGTGCCTGGTCCACGGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCCCTGGAGCTGCCCTTCAGTTTGTTGGCAGTTTGTGTTTTTTTTTTTTAAATCAAA
AAACAATTTTTAAAAAAAGCTTGAAAATGGATGGTTGGGTATTAAAAAGAAAAAAACTTAAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGCCAGACGT
TGAACGTGTTCCCTTCCCTGGCGCAGGGTGCAGGGTGTCTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTGTTCTGGGGAGGGAGGTTTTGTTGTTGTTGGGTTTTTGTGTTGCTTGTGTTCTTCTCCTCC
ATGTGTCTGGCAGGCACTCATTTCTGTTGGCTGCGCCAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGCCTCCATTGCCACCTCCCTCCTCGTGCCTGCCCTGCCCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTTGTTCCCACTCCCTGCCAGGGTGTGT
CCAGTGCCACCGCTGCCCTCCGCTTCCATCAGGCCCTGTCGCCACCTGGTCTTCATGAAGAGCAGACACTTA
GAGGCTGGCTGGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGGCTGGTGGTCCAAGGCCGGTTCCCGTCCCTGGCGC
CTGGAGTGCACACAGCCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTGTAGATCAGTCCGGTCCCCACCTT
AGAAGGGTCCCCGCCCTAGATCAATCACGTGGACACTAAGGCACGTTTAGAGTCTCTTGCTTAATGATTATGT
CCATCCGTCTGTCGTCGTCATTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAAATATGCACACTAG
CCTCTGACAACCATGAAGCAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTI IKVIKFILII CYTVY VVHNI KFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNNEWTL DKLQRQLTKNAQDKLELHLFMLSGIPDTVF DLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPAL AFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELH LTGNLSAENNR YIVIDGLRELKRLKVLRLKS NL SKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPH SIFSLHN LQEIDLKDNNLKTIEE IISFQ
HLHRLTCLKLWYNHIA YIPIQIGNLT NLERLYLNRN KIEKIPTQLFYCRKLRYLDL SHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALH LGNNVLQSLPSRVGE LTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCCTCTCCGT
CCCGCGGTGGTTGCTGCTGCCGCTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAAACCTTGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGAACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTGGGGGGT
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACAAAGCACTCCA
CGTCTACAATGGAGTCGAGTCAGAATTACACAGAGGCCACCTAGTTGTCTTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCTGGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTGTAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCATGGTCAGGAGGCCTG
GGTGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTCCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAECTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTGAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACACTAAACACATCCAGCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCCGGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

0 9 0 2 9 2 5 = 0 7 3 1 1 0

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPVRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGCCCCGGCGTGCAGGACCCCTGAGGAAGAGCTGAGTCACCTT
GCCCTGAGACAGCAGAAATGTGAAAGACTCTCGGAGCTGGTCAAGGCTGTGAGGATCCCAG
CTCTCCTCAATACGAAAATACCTGACCCTAGAGAATGTGGCTATCTGGTCAAGGCCATCCC
CACTGACCCCTCACACGGTGCAAAATGGCTCTGGCAGCCGGAGCCCAGAAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCACTATGTGGGAGGACCTACGAAACCATGTTGTAAGGTCCCCAC
ATCCCTACCAAGCTTCCACAGGCCTGGCCCCCATGTGGACTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCCTGTGATCCGTAAGCGATAACAATTGACCTCACAAAGACGTGG
GCTCTGGCACCAAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTCATGCGCCTTCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTGGACAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCACATCTCACCTGGCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGCTCACCTGCTTCGCCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTGGAAAGACACCAAGTTCCGCCCTACCTTCCCTGCCCTCCAG
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTAGCCCCACCTGCCACATCCAGTTACTTCAATGC
CAGTGGCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCATTCCATGGGTGTCGGAACCTCGGCCTCTACTCCAGTGGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCGCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCAGGGTTCTGCTCTGGCTGGGATCCTGTAACAGGC
TGGGGAACACCAACTCCCAGTTGCTGAAGACTCTACTCAACCCCTGACCCTTCTATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTGACTTCACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCCCAATAAGATGCTGTAACTAGCATTGGTGAATGCCCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGTTTCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTCTCAATCTTGTCTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTTGTCTTCTCTCATCAATTCTGCTTCTCAGTTACTCATTGTCCCTGGAACAAATCACTGACA
TCCATTGTAGATTGGCTCTCAGTTACTCATTGTCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVRSRPHYQLPQALAPHVDFVGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEFLQWML
LSNESALPHVHTVSYGDEDLSSAYIQRVNTELMKAAARGLTLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGGCGCCTCTCCGGGCCACACCTGCTGAGCGGCCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTCCTTC
TTCTTCTGCTCTGTGCTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTG
GCCTGCATAACCGCCTCCCTGCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTCTAAGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCAAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGGACTTCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACATGTCTCACAGCTGCCACTGCA
TACACGATGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGCGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTATTGGCATTTCAGG
GCACCAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAATCACTC
CTCTCAAATATGCCAGATTGCTATTGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGGTCCCTCTGGCAGCAATTAAAGGGCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCTTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATCTCACGTTTG
CAAACTTGATTTATTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

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FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTELQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA
AHCIHDGKTYVK
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKG
WIKGNA
NDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV
KDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVR
ITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCGAGCCTGCTGCCCTGCTCCCCGCCACCAGCCATGGTGGTT
CTGGAGCAGCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGTTGTGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAACGGACCCACACTGCGCAGGTTCTGCTCACCAAGCCGTGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGTCCCAGAAGGTGGTGTGCCCTGGTGAGC
CCCACCCCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCATGCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCATGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGACAGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTCGCGACCGCTCTGGTGGAGAAGATCGTCAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC
CCGCGCGCTCCTAGGGCGCAGCGGACGCGGGCTCGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGGCGGGCTCGGCGGTTCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCCAGGAAAGGAAACCCCTCCCCGACCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGCCCCGCCAC
GACTTCCGGCCCCGCCGGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTATT
AGGTATTTGTAACCTGCCACATATCTTATTATTCCCTCCAATTCAATAATTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAACFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS.

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCATGCA CGGCTCCTGCAGTT CCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCAAATGTCCCTCTGGCTACCACGTCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGTACTCCTTCCCTAGCAACGGGATTCCGGTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCGCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTCCTATCCAAAATCAGCAGACAAAGTGA CAGACAAAACA
AAAGTGCCTCTAGGAGCCCAGAGAACTCTGACCCCCAAGATGTCCTGACAGGGCAAG
GGAACCTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCCTCTGGTGTGGCTGGAATCTTCTGAATGGATACCAACTCAAAGGG
TGAAGAGGTCA GCTGTCCCTGTCATCTTCCCCACCCCTGCCCCAGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGAAGTGCACACC
GGGCCACACCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGAGTTGAGGGAGCT
CACTGCCCTACCTGGCCTGGGCTGTGCCCACACAGCATGTGCCTCTCCCTGAGTCGCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC
TTTGAAGTGGGGAGGCAGGGACGGAGGAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMILHMRWDEE
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGETPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSLPSLDEEPVTFPKS
THVPPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAAAGTCAGGCTTTCAATTGGGAAGCCCCCTCAACAGAACCGTCAATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTGTTCTCCCTTGCTTGCTTTCAACATTAGCAGACCCGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTCAAAGCCTCGAGAAGTGAACAACTGAACAACAAATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCGGCAAATATTACACTTCTCTCCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCACTGAAACTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCACACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAA
TTTGGGCAAACACTCCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT
GCCCAAACACTGCAACATCTCGAATTGAAACCGAAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTGG
TGCTCTGAACTCTGAAAGATGGAGTAACGAAACTATGGATGGAGCTTTGGGGCTGAGCAA
CATGGAAATTTCAGCTGGACATAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTTCATCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACCTTCATCACTTACAGGTTAGATGATTCAAGCTTCTGGCTTAAGCTTAAACTAAC
ACTGCACATTGGAACACAGACTCAGCTACATTGCTGATTGCCCCCTGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTCTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCAATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGAAAACAACCTT
TCAGAGCTTGTAAATGCCAGTTGCCCCATCCTCAGCTGCTAAAGGAAGAAGCATTGGTGTAGGCCAGA
TGGCTTGTTGCTGATGATTTCACAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTT
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGCAGTGAATTCCCCATGACTTTGCTTGGAAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAAGGGTGGCAGGTGATGGAGTATACAC
CATCTTCGGCTGCGCAGGGTGGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCATTGGTTC
ATCCTACTCTGTCAGGAACTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCATGGATCTCACCAT
CCGAGCTGGGCCATGGCACGCTGGAGTGTGCTGCTGTTGGGACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGCACAGACTTCCAGCTGCAACGGGAGAGACGCATGCATGTTGATGCCAGGATGACGTGTTCTTATCGT
GGATGTGAAGAGATAGAGGACATTGGGGTATACAGCTGCAACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGC
AACTCTGACTGTCCTAGAAAACACCATTTTGCGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGC
CGTCCCTACAGTCATGCTGGAGGAAGGCCCTCCCCCTAAACTGAACACTGGACCAAAGATGATAGCCATTGGTGGT
AACCGAGAGGCCATTGGCAGCAGGAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGTGATGCTGGAA
ATACACATGTGAGATGTCACACCCCTGGCACTGAGAGAGGAAACCTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTTGGGTGTCGTGATCATGC
CGTGGTTGCTGTTGGCACGTCACTCGTGTGGTGCATCATATACACACAAAGGCGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTATTGTGATCTCAGGGAACGTT
AGCTGACAGGCAGGATGGGTACGTCTCAGAAAGTGGAAAGCCACCAAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACACACATGACAGTAGTGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGGAGCTGC
CACAGATCTGTCCTTGTCCCTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCAGTCTGACCCAAAGAACAGTTTAATGGACCAACTGAGGCCAGTT
CATAAAGAAAAGGAGTGCCTACCCATGTTCTCATCCTCAGAAGAACCTGCCAACGGAGCTCAGTAATATATC
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCCCTTTAGATTAGTGCACATCCAGAGGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGGG
TACCTTGAAAGAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTGAGCC
AAGAGCCTTTATTGAAAGCTCATCTTCCCGAGCTTGGACTCTGGTCAGAGGAAGATGGAAAGAAAGGAC
AGATTTTCAAGGAAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGTCCAAATTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTATT
AAAGAGAGAGAATCTTATGTTAAATGGAGTTATGAATTAAAGGATAAAAATGCTTATTATACAGAT
GAACCAAAATTACAAAAGTTATGAAAATTTCATGTTGAAATGATGCTCATATAAGAATACCTTTAAACTA
TTTTTAACTTTGTTTATGCAAAAAGTATCTTACGTAATTAAATGATATAATCATGATTATTATGTATT
TTATAATGCCAGATTCTTATGAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCAATT
TTAAATAGAAGTTACTTCATTATATTGACATTATTTAATAAAATGTGTCACATTGAA

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FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRSLFIKASSMSHLQSLREVKLNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNISAIPPKMFKLQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE
FCQKLSLELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG
GEVMEYTTIILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGGISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKLNWTKDSPPLVVTER
HFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGETGNVRLSVIPTPTCDSPQMTAPSLLDDG
WATVGVIIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADI PSYLSSQGTTLAD
RQDGYSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNI
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG
AAGGATGCAGGACCGCAGCTTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTTGTGAGCCCTGGATCTAACACAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGGGGGGTTGGTGTGTTCTGACATAAATAATCTTAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAAGAACCGAGGATTACAAAGAAAAAGTATGTTCATTTTCTC
TATAAAGGAGAAAGTGAAGGAGATATTGGAAATGAAAAGTTGGGCTTTTAGTAAAGTAAAGAAACT
GGTGTGGTGGTGTTCCTTCTTGTGAAATTCCCACAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTGAACCGCCGAGATTGAGGATTGGGGAGAGAACCGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCACTGGATTTCCTCATCAACCTCCTTTAAAT
TTTATTCCCTTGGTATCAAGATCATGCGTTTCTCTGTTCTAACACCCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACGTGTTGAATTCCAGAAGGCCAACACAGATAAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTCT
GCTGGCTCTCAACTTCTGTGGTGGCTGGTCTGGTCCAGACCTGCCCTCTGTGCTCCTGCAGCAA
CCAGTTCAAGCAAGGTGATTGTGTCGGAAAAACCTCGCTGAGGTTCCGGATGGCATCTCCACCAACACAGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCACTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATGGAAATTGGGGCTTCAATGGTCTGGCAACCTCAACACTCTGGA
ACTCTTGACAAATCGTCTTACTACCATCCGAATGGAGCTTTGTATACTTGTCTAAACTGAAGGAGCTCTGTT
GCGAAACAACCCATTGAAAGCATCCCTTCTATGCTTTAACAGAAATTCCCTTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCTTGAAGGTCGTCCAATTGAGGTATTGAAACCTTGC
CATGTGCAACCTTCGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGATCTCTGGGAAATCA
TTTATCTGCCATCAGGCCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACAGTCCCAGAT
TCAAGTGAACGGAATGCCCTTGACAACTTCAGTCAGTAGGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCCTCATGCCCTTGCATCATCTAGAGCGATACTTACATCACAAACCTTGGAAACTG
TAACACTGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGACACAGCTTGTTGTGCCGGT
TAACACTCCTCCAACTCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGACACTCAATGTCAGTAAGGCATGGCAGCTGAGCTGAATGTGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCTAAATGGAAACAGTCATGACACATGGGGCTACAAAGTGCAGGATAGCTGT
GCTCAGTGTGGTACGTTAAATTCAAAATGTAACACTGTGCAAGATAACGGCATGTACACATGTATGGTGGTAA
TTCCGGTGGGAAATACTACTGCTTCAGCCACCTGAATGTTACTGCGAGCAACACTACTCCTTCTTTACTTT
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAAGGACACAGATAACAAATGTGGGCTCCACTCC
AGTGGTCAGTGGGAGACCACCAATGTGACCCACCTCTCACACCAACAGAGCACAAGGTGACAGAGAAAACCTT
CACCACCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTATGAAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCAACAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC
CATGAAAGCCACCTGCCATGCCCTGCTATCGAGCATGAGCACCTAAACTACTACATACAAATCTCCCTT
CAACACACAAACAGTTAACACAATAATTCAATACACAGTTGAGCTGATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAAACAAATCAAAAAAAA
GACAGTTATTAAGAACACAAATGACTGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTAAGAACACAAATGACTGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNADFNLQLSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNC
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVT
EGMAAE LKCRASTSLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTC
MVNSVGN TTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVD
WETTNVTTSLTPQ STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITL
MAAVMLVIFYKMRKQHHRQN HHAPTRTVEIIINV
DDEITGDTPMESHPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS VHEPLLIR
MNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACCGCTGCTCAAGCTGCAACTCTGTTGCAGTTGCAGTTCTGGTTCCCTCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACCGCACCGC
GAGGGCGGGCGTGCACCCCTCGGCTGGAAGTTGTGCCGGGCCCCGAGCGCGCCGGCTGGAGCTGGTAGA
GACCTAGGCCGCTGGACCGCGATGAGCGCCGAGCCTCCGTGCGCGCCGGCTGGAGCTGGTAGCGCTGTGC
GCGGTGCTGGGCGCGCTGGCCGCTGGGACTCGGACTGCAAGCTGGAGCTGGAGCTGGAGCTGGTAGCGCC
GAGGCCCATGCCACTACCTGCCGCTGCCCTGGGACTTAAGTCACAACAGATTATTCATCAAGGCAAGTTCC
CCCAGCCACTCCGCTCTGGGTCGCTGGACTTAAGTCACAACAGATTATTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCTTCAGAGAAGTGAAGACTGAACACAATGAATTGGAGACCATTCAGGAACTGGACCA
GTCTCGGCAAATATTACACTCTCCCTGGCTGGAAACAGGATTGTGAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTGGACCTAGCAGCAACAATATTTCAGAGCTCCAACACTGCATTCCAGGCCACAG
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGTATTGACAATTTGGCAACACAA
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCAAGATGTTAAACTGCCCAACTGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAATGTAGATGGACTGACATTCAAGGCCCTGGTGTCTGAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGGAAATTTG
CAGCTGGACCATAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCTGCAGGAACATT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTCCTGGCTTAAGCTTAACAAACTGCAACATTG
AACACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTCTGGCTTGACAAACTGAGGCAGCTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCACTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATTGCAATTAAATACA
TCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACACTTCAAGAGCTTGTA
AATGCCAGTTGCCCCATCCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGGCCAGATGGCTTGTG
GATGATTTCCCAAACCCCCAGATCAGGTTCAAGGCAAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTT
ATCTGCTCAGCTGCCAGCAGTCAGTGTGATTCCCAATGACTTTGCTGGAAAAAAAGACAATGAACACTG
GCTGAAATGGAAAATTATGCACACCTCCGGGGCAAGGTGGCAGGTGATGGAGTATACCACCATCCTCGGTG
CGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCCTTGTTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCACCGAGCTGGGCC
ATGGCACGCTGGAGTGTGCTGTTGGGACCCCAGCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC
TTCCAGCTGCACGGGAGAGACGCATGCACTGGTGGAGGATGACGTGTTCTTATCGTGGATGTGAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAGTATTCAAGCAATGCAACTCTGACTGTC
CTAGAACACCACATTTGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATGCCATTGGTGGTAACCGAGAGGCAC
TTTTTGCAAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGTGGAAATACACATGTGAG
ATGCTAACACCCCTGGCACTGAGAGAGGAACGTCGCCTCAGTGTGATCCCCACTCCAACCTGCACTCCCT
CAGATGACAGCCCCATGTTAGACGGATGACGGATGGGCACTGTGGGTGCTGATCATAGCCGTGGTTGCTGT
GTGGTGGGCACTGCACTCGTGTGGGTGCTCATCATATAACCACACAAGGCGGAGGAATGAAGATTGAGCATTAC
AACACAGATGAGACCAACTTGCACAGATATTCTCTAGTTATTGTCATCTCAGGGACGTTAGCTGACAGGAG
GATGGTACGTTCTCAGAAAAGTGAAGCCACCAAGTTGTACATCTCAGGTGCTGGATTTCCTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTTGAAGCTGCCACAGATCTGTC
CTTTGTCGGTTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTTGATGGCTCAGATCCTTTGAAACA
TATCATACAGGTTGCAGTCTGCCACAGAACAGTGTGTTAATGGACCACTATGAGGCCAGTTACATAAAAGAAAAAG
GAGTGTACCCATGTTCTCATCCTCAGAAGAAATCCTGCCACAGGCTTCAAGTAAATATGTCGGCTTACAT
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAAATGAAAATCTGTCATAACAGTCC
TCTTAGATTGTCGAAATCCAGAGCCAGCGTCGGTCTCGAGTAATTCTCATGGTACCTTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTAT
TTGAAAGCTCATTCTCCCCAGACTGGACTCTGGTCAAGAGGAAGATGGGAAAGAAAGGACAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTAGAAAACACTACAGGACTCCAAATTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACACTACCTCAAGTGAACCTTTATTAAAAGAGAGAAT
CTTATGTTTTAAATGGAGTTATGAATTAAAAGGATAAAATGCTTATTATACAGATGAAACAAAATTAC
AAAAGTTATGAAATTAACTGGGAATGATGTCATATAAGAATACCTTTAAACTATTTTAACTTTG
TTTATGCAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTATGATTGTTATAATGCCAGA
TTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTTTAAATAGAAGTT
ACTCATTATATTGCACTTAAATTAATGTCATTGAAAAAAAAAAAAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQLSQLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRISSAIPPKMFKLSQLQHLELRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGGLSNMEIQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSLEDLTFNHLSDLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNNIEIS
WTIEDMNGAFSGLDKLRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLPQWVAEENNQSFVNASCAPQLLKGRSIFAVSPDGVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLRTVKGETAVLQCIAGGSPPPKNWTKDDSPVVTERHF
FAAGNQLLIIVDSDVSDAGKYCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTLADRO
DGYVSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCRSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGGCTCGCGGAGAGCGCCCCAGCTTGAATGGAAGGAGCCCGAGCCCGGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTCGGCCGTGCCCCCTGGCGCCGCTCGGCCGGGGCGCAGCAGGGAAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCACACTGGTGTGAACCGGGAGAGCCCCCTGGGTGGTCCCCTATCCCTCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGCAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG
GCGCACAGCATTGGAGTTACAGATTTAACAGATACCAATGGAAGGCGAGGAGGCAGAACAGCCTGCCGGT
TCCATCAGCCCTGGCGCCAGGCACATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGGCCGGTGTGC
TGCTCCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCCTGAGGGCCCCAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGAGGCCGTGTGGACTGAGCCCTGAGG
AGCCCGGGCTGGCCAGCCGGTCACTGGCCCCGGACTGTGCTGTGCTCCAGGGGGCTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCGGGGACCTGCTGAGCACACCAACCTATCTGAGAACACAACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGCTGCACCGGCTGGAGACACTGAACTGCAAACCAAAACAACCAGC
CTTCCCGAGGGCTCCAGAGAAGGGCTTGAACATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAAGC
TGACCTTGGCACCCCGCTTCTGCCAACGCCCTGATCAGTGTGGACTTTGCTGCCAACATATCTCACCAAGATCT
ATGGGCTCACCTTGGCCAGAACGCAAACCTGAGGTCTGTGTACCTGCACAAACAAGCTGGCAGACGCCGGC
TGCCGGACAAACATGTTCAACGGCTCCAGCAACGTCGAGGTCTCATCCTGTCAGCAACTTCCCTGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAAACAAGCTGGAGAAGATCCCCGGGGC
TCAGCGAGCTGAGCAGCTGCCAGCTATAACCTGCAAGAACAAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTCTGGAAGCTCTCAGCTGGAGTACCTGGATCTGTCAGCAACAAACCTGTCAGGGTCCAGCTGGCTGC
CGCGCAGCCTGGTGCTGCACTGGAGAAGAACGCCATCCGGAGCGTGGACGCCAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCAAGCAACCAGCTGCCGGAGCAGGGCATTCCACCCACTGGCCTCAGGGC
TCAAGCGTTGCACACGGTGCACCTGTACAACAAACGCGCTGGAGCGCTGCCAGTGGCCTGCCCTGCCGCGTGC
GCACCCCTCATGATCTGCAACACCAGATCACAGGCACTGGCCGGAAGACTTGGCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACAGGCCACAGGTGCACCGCAGCCTCCGCAAGCTGCCCTGCTGC
GCTCGCTGGACCTGTGCTGGCAACCCGGCTGCAACCGCTGCCACCTGGGCTGCCATGGCTCAGCTGCGTGAAGG
TCAAGCGCAATGAGCTGGCTGCTTGGCACGAGGGGGCTGGCGCATGGCTCAGCTGCGTGAAGCTGTACCTCA
CCAGCAACCGACTGCCAGCCGAGCCCTGGGGGGCTGGCTGGGACCTGCCCATCTGCAAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCGAGTCACTTGAGTACCTGCAAGAACACA
AGATTAGTGCCTGCCCCCAATGCCCTCGACTCCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTCCGGAGGTGAAGCACCTGCAAGGTCTTGGACATTGAAGGCAACT
TAGAGTTGGTGAACATTCCAAGGACCGTGGCCGCTTGGGAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGGGACTCTTCTGC
AGCACACGCCCTGTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGGCTGACACACTCTCATATCCCCACCCCTCCACGGCGTGTCCCAGGCCAGACACATGC
ACACACATCACACCCCTAAACACCCAGCTGCCACACACAACACTACCCCTCAAACACCACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAAAGGGCTGCCCTGCCACACACAGGCC
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAGCTATGCCACAGACAGCTCTGCCAGCCAGAATGCCATAGCAGCTGCCGTGTGCC
GTCCATCTGTCGTCGCTCCGTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCCACCCCT
GGAACTCACAAAAGCTGGTTTATCCTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCTGGCC
TGGCCCAACCTGCTCCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCGTGCCAGGCCCTGGCAGGACA
CAGGCACTTTCAATGGGAAGGCCAGTGGAGGAGGAGGAGGAGGCCCTGGGTGCTGCTGGGCTTGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGCTGAGCCAGGGAGGAAGGAGGCCAGCTGCAACCTAGGAGACACCTT
GTTCTCAGGCTGTGGGGAGTTCGGGTGCCCTTATTTTATCTTCTAAGGAAAAAAATGATAAAAT
CTCAAAGCTGATTTTCTGTTAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCCAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAEEEPVLVLSPEEPGP GPAVSCP RD CACS QEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKA FEHLTN NYLYLANNK
LT LAPRFLPNALISVDFA ANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EV LI LSSN FFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ET FWKLSSLEYLDLSSNNLSRVPA GLPRSLVLLHLEKNAIRSDANV LPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITS PQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQ LLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCCGCAGCAGACCTGCTCCGGCGCGCTGCCGCTGTCCCTCCGGAGCGGCAG
CAGTAGCCCCGGCGGGCTGGGGTCTCTCGAGACTCTCAGAGGGCGCCTCCCACATGGGATTTCCTCTGGCGTGGT
CAACCTGTTCTCGCGGCCACTCGCCTGCCAGGACCCGCTGCCAACATGGGATTTCCTCTGGCGTGGT
GCTGGTATCTCGCTCACCTGCAGGGCCGCGAGTTGACGGGAGGTGCCAGGAAATAGTGTATCGAT
TGGCCTATGCTGTTATGGTGGGAGGAATTGACTGCTGCTGGGCTGGGCTGCCAGTCTGGGACAGTGTACGCC
TGTGTGCCAACACGATGCAAACATGGTGAATGTATGGGCAAACAAGTGAAGTGTACCTCTGGTATATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGGCCCCGGCCCTGTAAGCAGGGTGCATGAACACTTA
CGGCAGCTACAAGTGCTACTGTCTCACCGGATATGCTCATGCCGGATGGTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACGTCACTGGCTGTGATGTTGTTAAAGGCAAATACGGTGCAGTGCCTGCCATCCCCCTGGCCT
GCACCTGGCTCTGATGGGAGGACCTGTGATGATGAAATGCTACAGGAAGAGCCTCTGCCCTAGATT
TAGGCAATGTTGTCACACACTTTGGGAGCTACATCTGCAAGTGTCAAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCATGACATAGACGAATGCTACTGGTCAGTATCAGTGAGCAGCTTGCTCGATGTTAA
CGTACGTGGGCTTACAAGTCAAATGTAAGAAGGATACCAGGGTGTGGACTGACTTGTGTATATCCCCAA
AGTTATGATTGAAACCTTCAGGTCAAATTCAATGTACCAAAGGGAAATGGTACCTTTAAAGGGTACACAGGAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCTCTATCATTACCAA
CAGGCCTACTCTAACGCAACAAACAAGACCTACACCAAAGCCAACACCAATTCTACTCCACCAACACCAC
CCTGCCAACAGAGCTCAGAACACCTTACACCTACAACCCCCAGAAAGGCAACCACGGACTGACAACATAGC
ACCAAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACACCTCAGAAACCCAGGG
AGATGTTGTTCACTGTTCTGGTACACAGTTGTAATTTCGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTGGTGTACCTCTCGGCCGCTCATGCATTCAAGGGACCTGTGCCTGTATTAGGCA
CAAGGTGACGGGGCTGCACACTCGCACACTCAGGTGTTGTGAGAAAACAGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAAATGGTGGCATGGCTGGGAAACACAGATCACCTTGCGAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACCTGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCATGATGGTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GCCATTGTTAGAATACTCTAACAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTCTCTAAAGGAAATTAGA
TAAAAAATTGCTATTAAAGATGGTAAAGATGTTCTAACCAAGGAAAGTAACAAATTATAGAATTTCACCAA
AGATGTTTGTGATCCTACTAGTAGTATGCACTGGGAAACTTAAAGGAAACTTAAATTTGGACAAGGCTTAATTAGG
CATTTCCCTCTTGACCTCCTAACGGGATTGAAAGGGGAAAGAGGCCAACAAATGCTGAGGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAGGAAACTATTATTCACCATGAGAGTATGATGGAC
AGATATTAGTATCTCAGTAATGCTTAGTGTGGCGGTGGTTCAATGTTCTCATGGTAAAGGTATAAGGCC
TTTCATTGTTCAATGGATGATGTTAGATTTTTTTAAAGAGATCCTCAAGGAACACAGTTCAGAGAG
ATTTCATCGGGTGCATTCTCTGCTTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGGCCCTGCC
ACACCGGCAGACCTTCTCACCTCATCAGTATGATTGAGTTCTCTTATCAATTGGACTCTCCCAGGTTCCAC
AGAACAGTAATTTGGAAACATAGGTACAATAGAAGGTCTCTGTCATTAAACCTGGTAAAGGCAGGGCTGG
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATGGCTGTAGATCCATTAAATGGTCAATT
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAATAATGAAAATTACTTGTATGCAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTATTATTAAATGTTT
CTAAAATAAAATGTTAGTGGTTTCCAAATGCCCTAATAAAACAATTATTGTAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE C1GPNKCKCHPGYAGKTCNQDLNECGLKPRPC KHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGR TCDVDECATGRASCPRF RQC
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFAR CYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGN NWIPDVGSTWWPPKTPYI PPIITNRP
TSKPTTRPTPKPTPIPTPPPPLPTELRTPLPPTT PERPTT GLTTIAPA AASTPPGGITVDN
RVQTDPQKPRGDVF SVLVHSCNF DHGLCGWI REKDNDLHW EPIRD PAGG QYLT VSAAKA PGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGA ALWGRNGGHGWRQTQI
TLRGADIKSE SQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGCAACAGGTGCTGCTCGGGCTGA
AGGTGACAGTGCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA
ACAATGCCAAATACTTACTGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAAATACC
AACACAAGTCACCATGATGCCACCCAATGCATCTGTCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAAATGGAACCTATCTGCCAGTCA
GAAGATAACAAGTCACGGTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCACTCCCT
CTGGGCTGTGGAGTATGTGGGAACATGACCCGTACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTC
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT
GCCTGGTGGAGGAACCCGTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTG
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATACTGGAAATATCACTATTGATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAAATCAACCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGGCAAGATTGCACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTAGAGT**GA**ACTTCTATGG
GCTAAACAGTACATTGAGTGAAATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAACCCAGGACCAACACCTCTACTCATTATTCTTACA
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATAACAAATGTCTT
GTGCAACAGAAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTCCCTCATAAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGCTCACCTACAAA
TGTGGAAACCTTACATTGTTGATTTTCAGCAGACTTGTGTTTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTTCAGGAAATTCTATCTTGTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAACAAAACAACTATGCCTCTCTTTTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGTAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIWIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSAQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKGPRLEVASEKVAQKTMGYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGCGAAATGGCGCCCTCCGGGAGTCTTCAGTTCCCTGGCAGTCCTGGTGTGTT
GCTTTGGGGTGCTCCCTGGACGCACGGCGGGAGCAACGTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAGGAGACTGGATGATAGAATTTTATGCCCGTGGTGCCTGCT
TGTAAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG
GTTGGTCCAGGTTCTGTTGATGAGTAGTATGTCAGCACTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAAGACCTTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCTTCAAAAAGGGCAGACCACAGCCATACCCATACCCTTCAAAAAAAT
TATTATCAGAACTGCACAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAAACAACAAAGACTTCCACAGAATGC
CATAAGACAACGCTCTGGTCCATCATTGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATATTGCAAGGGTTCAGTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAGTTGAAATATGATTAAGCACAGTATGATG
GTTAAATAGTCTCAATTTTGAAAAATCGTCCAAGCAATAAGATTTATGATATTGTATTG
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAGTATTGCATTAT
TGAGGTATTTAAGAAGATTTTAGAGAAAATTACTCTCATTTGATATAATTTTCTCTG
TTCACTGTGTAAGAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTATTCAGACATTCGGGCTTTAGAGGTATATTCCAAAATTCCCTTGT
ATTTTTAGTTTATGCACTAAAATAAACTACCTTACATTAATTACAGTTTCTACACA
TGGTAATACAGGATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTTGATTC
CAACAAAGTTGATTCTCTGTATTTTCTTACTACTATGGGTTACATTTTTATTTT
CAAATTGGATGATATTCTGGAAACATTTTTATGTTAGTAAACAGTATTTTTTGTT
GTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGTAATTAAAATT
TTGGCCACTTTTCAGATTTCATCATTCTGCTGAACTTCAACTTGAAATTGTTTTT
TTCTTTGGATGTGAAGGTGAACATTCTGATTTTGCTGTGAAAAGCCTTGGTA
TTTACATTTTGAAAATTCAAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTTCTTGTATATGTCTAAATGTATTTTGCTCTCATATACAGAAAGTTCTTAATTGAT
TTACAGTCTGTAATGCTGATGTTAAAATAAACATTTTATTTTTAAAAGACAA
ACTTCATATTATCCTGTTTCTTCCGTACTGGTAATTGTGTCGGGATTCACAGGTAAAAG
GTCAGTAGGATGGAACATTTTAGTGTATTTTACTCCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGGAAATCATAAAATACAATGAATCACTGACCATTACGTAGTAGAC
AATTCTGTAATGCCCTTCTTCTAGGCTGTGTAATTGTGGGATTCACAGGTAAAAG
TATCGTAATACAAGTTTCTTAAAGCCCTTCCTTAGAAATTAAATATTGTACCATT
AAAGAGTTGGATGTGTAACTTGTGATGCCTAGAAAATATCCTAAAGCACAAAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GGAGTGTCCAGCTCGGAGACCGTGATAATTGTTAACTAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAACCGCAAGCAGTGCTAACCGACTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGACACTTCCCTCTGTGACCATTGAAACTCTGGGTGTC
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGAGGCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCACTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GTTTTATCGCCAACCTCTGTGAGCGGCAGTTCTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCGCTCGGCCTACAATGAAGGGACTATTATCATAACGGTGTGAGTGGACTGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCTTCAGTTGGGTGATCTGCACCGTGCCTGGAGCTACCCGCCCTGCTC
TCCCTTGACCCAAAGCCACGAACGAGCTGGAGGAATCTCGGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAACGCTGAGCTAGCAACCCAGAAGGCA
TCTATGAGAGGGCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTGTGCTGGG
GAGGGTGTCAAACGTGACACCCCGTAGACAGAACGAGGCTTTCTGTAGGTACCAACCATGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCTTCAAAGAGGAGGACGAGTGGACAGCCGCACA
TCGTCAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGCACGAGCCACCGTTCGTGTACCCAAAGACAGGAGCCTCACTGTGCCAGCTA
CCGGTTTCAAAGCTCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTCTCTAGGCGACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGCGGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCCCTGCC
TGTGCTTGTGGCTGCAAGTGGCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAACGTTTGACATCCCTTCTGTCTCTCCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTCAAGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAATGTCCTACCAAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSHVQAEFFTSIGHMTDLIYAEKELVQLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEATTTKSQVLDLYSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAEELATPEGIYERPVVDYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPQOLLIAPKEEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEVDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCTTTAGTGGAAAGACAGACCATAATCCAGTGTGAGTGAATTGATGT
TTCATTTATTACCGTTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGATGCTGGTCTGGAAGCCAGCGGGCTTGCTCTGTCTTGGCCTCATTGACCC
CAGGTTCTGGTTAAAACGTAAAGCCTACTACTGGCTGGTGCCTCAATCCATTGATCCTGAGGCTGTGCC
CCTGGGGCACCCACCTGGCAGGGCCTACCACGACTTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTCTCTGGGGTGCAGCCTGAGCCTCCCTGCGGTTTCTGGATCCAGGGGGAGGGAGAAG
ATCCCTGTGTCAGGGCTGTAGGGGAGGAGGGCCACAGAACATCCAGATTCGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCGGATTGCCCCACTACAGGGACCCAAACAAGCCTACAAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGACTGGGCTCCCGTGAGCGGTTGCTGGTGCCTGACCTCCGAGCTACACTGTCCA
CTTGCGCTGGCTGTGAACCGTACGGTGGCCCATACTTCCCTCGGTTACTCTACTTCACTGGGAGCGGGGG
CCCGGGCTCCAGCAGGGATGCAAGGTGGTCTCATGGGATGAGCGGGCCCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGCGACTACGACTGGTTCTCATCATGCAAGGATGACACATATGTGCAGGCC
CCCGCCTGGCAGGCCCTGGCTGGCACCTCAGCATCAACCAAGACCTGACTTACGGCGGGCAGAGGAGTTCATGG
GCGCAGGCGAGCAGGCCGGTACTGTCACTGGGGCTTGGCTACCTGTCACGGAGTCTCCTGCTTCGTCTGC
GGCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGCCGCTCTGACGAGTGGCTGGACGCTGCCCTATTG
ACTCTCTGGGCGTCGGCTGTCTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACTGGCCAAAAATAGGG
ACCTGAGAAGGAAGGGAGCTCGGCTTCTGAGTGCCCTCGCCGACCTGACGGCTTCCGAAGGTACCCCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACAACTGAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACCACACTCTCGCTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCTGTCAGATGGGG
CTCCAAGTGCCCACTACAGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCGCTATCAGCCCCGCTGCGCTTCCAGAACAGCAGCAGTCTCAACGGCTATCGGCCTTCGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTGTTGGATGTGACACAGCGTGGGACCGGGCCCTGGCTCGCA
GGTCAGCCTGCTGCCACTGAGCCGGGGTGGAAATCTACCTATGCCCTATGTCACTGAGGCCACCCAGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAAGCCCCGGCTTCTGAGGCGTTGAGCCAATGTCC
TGGAGCCACGAGAACATGCAATTGCTCACCTGTTGCTCTACGGGCCACGAGAACGGTGGCCGTGGAGCTCCAG
ACCATTTCTGGGGTGAAGGCTGCAAGGCCCTTCCCAGGTGCACTCATGGACGTGGCTCGAAGAACACCCCTGTGGACACTCT
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCACTCATGGACGTGGCTCGAAGAACACCCCTGTGGACACTCT
TCTCCTTACCAACCGTGTGGACAAGGCCCTGGGCCGAAGTCTCAACCCGCTGCGCATGAATGCCATCTGGCT
GGCAGGCCCTTCTTCCAGTCCATTCCAGGAGTTCAATTCTGCCCTGTCAACACAGAGATCACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTCTGGTGTGACCCCTCCGGGGGCTCCTATAGGGGGAGATTG
ACCGCAGGCTCTGGGAGGGCTGTTCTACAACGCTGACTACCTGGCGGCCGAGCCGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCCTGGAGGGGCTGGAGGTGATGGATGTTCTCCTGGCTCAGGGCTCC
ACCTCTTCTGGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG
AACTCTACCACCGCTGCCGCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCATAGCACTTAGCCGCTGGGGCCCTAACCTCATTACCTTCTGTCTGCCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPD
SRARLDQSDEFKPRIVPYYRDPNPKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEFIGAGEQARYCHGGFGYLLSRSLLLRLPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLPEGEAGLSWPVGLPAPFTP
HSRFEV LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTL DLLC VCTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLP
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKA
AAAEELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTWTRPGPEV
LNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPI
GGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSP
RLSEELYHR
CRLSNLEGLGGRQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGC CGGCTGCCTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACCAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC TG
GTTCTCCTTGCACGCCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGTATACCGCCTAGGGCATTTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTAACATACATACCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAACACATGAACACATTGTAAATG
TGTTGGAAAGAAGTGTAAAGAATAATAATTGCAAATAACTATTAAATAATATTAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACATTAGCTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCTCTCAAAATGTACAACACTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDQQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCGCGCTGCCGCTGGCCCCTCAGCAACCCCGACATGGCGCTGAGGCAGGCCACCGCGAC
TCCGGCTCTGCCCTGCCCTGACTTCTTCCTGCTGCTGCTTTCAAGGGCTGCCGTAGGGCTGTAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGAAACTGTCTTGATCATTACGGATTGCG
AGACAAGTGAACCCAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAAGGGAGACTTGGCGGGTCTGCAAGAAATACTGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCGCTCGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCTGAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCCGCCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTCTTCACTTAAACTCTGAAACAGGCACTTGGTGTTCACTGCTG
TTCAACAAGGACGACTCTGGCAGTACTACTGCAATTGCTTCAATGACGCCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGAATTATTGGGGGGTCTGGTTGTCTGTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTCATCAACAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAAGATGGAGTTAATCACATCCGACTGACGAGGAGGGCAGTTCAGACACAAAGTCATCGTTT
TGATCTGAGACCCCGCGGTGAGAGCGCACAGAGCGCACGTGACATACCTCTGCTAGAAAATCCTGTC
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTGCTTGGCCAAAGTTGACCA
CTACTCTTCTACTCTAACAGCACATGAATAGAAGAATTTCCTCAAGATGGACCCGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGTCTTAATCTGTTCTGGCTGATTCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTACGTAACGCCGTGCTGGCCCTGTGAAGGCAGCATGTTACCAACTGGTC
CAGCAGGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGACCCA
GAAAAGGCTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTG
TGATCGGTGTTGCACTGAGTTGGGATCAGCATTTGTTAAACCAACAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTGCTGAGGAACCCCTGCTGTCCAACAGGGTGTCAAGGATTTAAGGAAA
ACCTCGCTTCTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTCTATGGGCTTGTATTAAATTAAATT
TACATCTAAATTGGCTAAGGATGTATTGATTAGAAGAAATTCTATTAAACTGTAATATATTGT
CATACAATGTTAAACCTATTGGGATGGCTAAGGTTCAACTTAAGGTTAGAAGTCTAACGACTAGTGTAAAT
TGGAAAATATCAAATTAAAGGTTACCAAGGAATCCTCTATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTTACGCTTTCACAAGGAACTCATACTGCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAAGCAATGTTGAAATCAGTTGCTCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGA
GCCTCTTCTGAGATGACTAGGACAGTCTGTAACCCAGAGGCCACCCAGAACGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCCTGGGGTGCCTGGCCAGGCGCCCCCGCTAGCTACTGTCCTGCTGCTGCA
GCCATCCTTGGGCCCTGGCAGTGGCTGTCTTCAAGTGGCTTACTCACGTGGCCCTTGCTTCA
TCTCAGGTGGGACTGCAGGGACACTGGTGTCTTCAAGTGGCTTGGGCTCTGTAACAGACCTCT
TTTGGTTATGGATGGCTACAAAATAGGGCCCCAATGCTATTGGTTAAAGTTGTTAAATTATTTGTT
AAGATTGTCAGGCAAAGGCAATTGCGAAATCAAGTCTGCAAGTACAATAACATTAAAAGAAAATGGAT
CCCACGTTCTCTTGCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTCGATTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGGCCAGGTGAAAGGCCCTGGCGGGAGGAAG
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGCCAGACACTGCTCCCATT
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC
GCCGTGCTGGACTCAGGACTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTC
GAATGGCTCTCACTCACCTGCTTTCACTTCAAGCTTCAAGTGGTTTTTAACTTTGACAGCTTTTT
AATTGCAATCATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGGCAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCCTGGTGTCTGCTGCATGGCATTGGATGCTTAGCATGCAAGTTC
CCTCCATATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCA
TCTGGTTGTCATAGTGTAGGGTAGCCTTATTGCCCTCTTCAACCTAAACCTCTACACTAGTGC
TGGGAACCAAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGC
CTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTTAAGATATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

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FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267